

SUPPLEMENTAL TABLE 2. Peptide/Protein Identification Data.

Entry Q#	UniProt Protein ID	UniProt Protein Entry	Gene Name	Protein Name	Protein Probability	Protein Coverage (%)	# of Unique Sequences	# of Identified Peptides	Total # of Identified Spectra
						Peptide Sequence	Peptide Charge	Peptide Probability	Number of Spectra
Q51-1	E9PNH7	E9PNH7_HUMAN	CRYAB	Alpha-crystallin B chain (Fragment)	1.0000	15.09	2	2	2
Q51-2	A0A024R3B9	A0A024R3B9_HUMAN	CRYAB	Crystallin, alpha B, isoform CRA_c	1.0000	14.81	2	2	2
						FSVNLQDVK	2	0.9658	1
						HFSPEELK	2	0.9879	1
Q52-1	A2A3R5	A2A3R5_HUMAN	RPS6	40S ribosomal protein S6	0.9863	6.88	1	1	2
Q52-2	A2A3R7	A2A3R7_HUMAN	RPS6	40S ribosomal protein S6	0.9863	16.48	1	1	2
Q52-3	P62753	RS6_HUMAN	RPS6	40S ribosomal protein S6	0.9863	6.02	1	1	2
						MATEVAADALGEEWK	2	0.9863	2
Q53-1	P36915	GNL1_HUMAN	GNL1	Guanine nucleotide-binding protein-like 1	0.9999	4.94	2	2	3
Q53-2	A2AB27	A2AB27_HUMAN	GNL1	Guanine nucleotide-binding protein-like 1 (Fragment)	0.9999	11.36	2	2	3
						EQVLQPVSAELLEDIR	2	0.9952	1
						EVYQPGSVLDFFPR	2	0.9883	2
Q54-1	Q9UM22	EPDR1_HUMAN	EPDR1	Mammalian ependymin-related protein 1	0.9973	10.27	2	2	2
Q54-2	A4D1W8	A4D1W8_HUMAN	UCC1	Ependymin related protein 1 (Zebrafish), isoform CRA_b	0.9973	6.69	2	2	2
						ALLSYDGLNQR	2	0.9669	1
						SVETWIGIVTVK	2	0.9191	1
Q55-1	A6NC17	A6NC17_HUMAN	MARS	Methionine-tRNA ligase, cytoplasmic	1.0000	3.62	2	2	3
Q55-2	B3KVK7	B3KVK7_HUMAN	MARS	Methionine-tRNA ligase, cytoplasmic	1.0000	4.21	2	2	3
Q55-3	P56192	SYMC_HUMAN	MARS	Methionine-tRNA ligase, cytoplasmic	1.0000	2.56	2	2	3
Q55-4	H0YHV5	H0YHV5_HUMAN	MARS	Methionine-tRNA ligase, cytoplasmic (Fragment)	1.0000	9.87	2	2	3
						GFVLQDTTVEQLR	2	0.9703	1
						WFNISDFIGR	2	0.9993	2
Q56-1	P08865	RSSA_HUMAN	RPSA	40S ribosomal protein SA	0.9150	5.76	1	1	1
Q56-2	C9J9K3	C9J9K3_HUMAN	RPSA	40S ribosomal protein SA (Fragment)	0.9150	6.46	1	1	1
Q56-3	A6NE09	A6NE09_HUMAN	RPSAP58	40S ribosomal protein SA	0.9150	5.76	1	1	1
						AVNAIENPADVSVISR	2	0.915	1
Q57-1	A6NFN2	A6NFN2_HUMAN	ABI1	Abl interactor 1	0.9993	2.16	1	1	1
Q57-2	FSH1G9	FSH1G9_HUMAN	ABI1	Abl interactor 1	0.9993	2.79	1	1	1
Q57-3	FWA55	FWA55_HUMAN	ABI1	Abl interactor 1	0.9993	2.6	1	1	1
Q57-4	FWA56	FWA56_HUMAN	ABI1	Abl interactor 1	0.9993	2.28	1	1	1
Q57-5	Q8IZP0	ABI1_HUMAN	ABI1	Abl interactor 1	0.9993	2.17	1	1	1
Q57-6	Q8IZP0-10	ABI1_HUMAN	ABI1	Isoform 10 of Abl interactor 1	0.9993	2.84	1	1	1
Q57-7	Q8IZP0-11	ABI1_HUMAN	ABI1	Isoform 11 of Abl interactor 1	0.9993	3.34	1	1	1
Q57-8	Q8IZP0-12	ABI1_HUMAN	ABI1	Isoform 12 of Abl interactor 1	0.9993	2.22	1	1	1
Q57-9	Q8IZP0-2	ABI1_HUMAN	ABI1	Isoform 2 of Abl interactor 1	0.9993	2.47	1	1	1
Q57-10	Q8IZP0-3	ABI1_HUMAN	ABI1	Isoform 3 of Abl interactor 1	0.9993	2.43	1	1	1
Q57-11	Q8IZP0-4	ABI1_HUMAN	ABI1	Isoform 4 of Abl interactor 1	0.9993	2.44	1	1	1
Q57-12	Q8IZP0-5	ABI1_HUMAN	ABI1	Isoform 5 of Abl interactor 1	0.9993	2.31	1	1	1
Q57-13	Q8IZP0-6	ABI1_HUMAN	ABI1	Isoform 6 of Abl interactor 1	0.9993	2.29	1	1	1
Q57-14	Q8IZP0-7	ABI1_HUMAN	ABI1	Isoform 7 of Abl interactor 1	0.9993	2.61	1	1	1
Q57-15	Q8IZP0-8	ABI1_HUMAN	ABI1	Isoform 8 of Abl interactor 1	0.9993	2.8	1	1	1
Q57-16	Q8IZP0-9	ABI1_HUMAN	ABI1	Isoform 9 of Abl interactor 1	0.9993	2.29	1	1	1
						ALIESYQNLTR	2	0.9969	1
Q58-1	Q13813-2	SPTN1_HUMAN	SPTAN1	Isoform 2 of Spectrin alpha chain, non-erythrocytic 1	1.0000	2.46	6	6	9
Q58-2	Q13813-3	SPTN1_HUMAN	SPTAN1	Isoform 3 of Spectrin alpha chain, non-erythrocytic 1	1.0000	2.49	6	6	9
Q58-3	A6NG51	A6NG51_HUMAN	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	1.0000	2.46	6	6	9
Q58-4	Q13813	SPTN1_HUMAN	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	1.0000	2.47	6	6	9
						AALLELWELR	2	0.9996	2
						AALLELWELRR	3	0.9578	1
						DVDEIEAWISKK	2	0.9931	1
						ELPTAFQDVETTR	2	0.9889	3
						LQSHSPESAEGLQEK	2	0.8888	1
						SEETIESAFR	2	0.8149	1
Q59-1	A6NKB8	A6NKB8_HUMAN	RNPEP	Aminopeptidase B	1.0000	11.62	6	6	8
						AEEGPPPGAGSR	2	0.9907	1
						AFELHLHL	3	0.8938	1
						CLEPEGAELR	2	0.8422	1
						GLSGTAVLDLR	2	0.9983	2
						ISTILFGAAYTCLEAATGR	3	0.9104	1
						LQVLLTYR	2	0.9681	2
Q510-1	A8MU3	A8MU3_HUMAN	RPL23A	60S ribosomal protein L23a	0.9969	12.89	2	2	2
Q510-2	K7EMA7	K7EMA7_HUMAN	RPL23A	60S ribosomal protein L23a	0.9969	35.71	2	2	2
Q510-3	P62750	RPL23A_HUMAN	RPL23A	60S ribosomal protein L23a	0.9969	16.03	2	2	2
Q510-4	H78Y10	H78Y10_HUMAN	RPL23A	60S ribosomal protein L23a (Fragment)	0.9969	15.82	2	2	2
Q510-5	K7EYV9	K7EYV9_HUMAN	RPL23A	60S ribosomal protein L23a (Fragment)	0.9969	14.71	2	2	2
Q510-6	K7ERT8	K7ERT8_HUMAN	RPL23A	60S ribosomal protein L23a (Fragment)	0.9969	14.29	2	2	2
						LAPDYDALDVANK	2	0.9543	1
						VNTRPDPGEKK	2	0.9315	1
Q511-1	ABMW50	ABMW50_HUMAN	LDHB	L-lactate dehydrogenase (Fragment)	1.0000	10.34	2	2	2
						IVVVTAGVR	2	0.9019	1
						SLADELALVDVLEK	2	0.9993	1
Q512-1	ABMX94	ABMX94_HUMAN	GSTP1	Glutathione S-transferase P	1.0000	21.26	4	4	13
						ASCLYGQLPK	2	0.9996	3
						FQDGDGLTYNSNTILR	2	0.9997	6
						PPYTVVFPVR	2	0.9984	3
						SCLYGQLPK	2	0.983	1
Q513-1	Q99733-2	NP114_HUMAN	NAP114	Isoform 2 of Nucleosome assembly protein 1-like 4	1.0000	7.25	2	2	4
Q513-2	Q99733	NP114_HUMAN	NAP114	Nucleosome assembly protein 1-like 4	1.0000	7.47	2	2	4
Q513-3	ABMXH2	ABMXH2_HUMAN	NAP114	Nucleosome assembly protein 1-like 4 (Fragment)	1.0000	17.95	2	2	4
Q513-4	C9JZ17	C9JZ17_HUMAN	NAP114	Nucleosome assembly protein 1-like 4 (Fragment)	1.0000	10.07	2	2	4
						FYEEVDHLR	2	0.9994	2
						NVDMLSLVQYDEPIIK	2	0.9987	2
Q514-1	ABMYE6	ABMYE6_HUMAN	ITGB2	Integrin beta	0.9945	3.37	2	2	2
Q514-2	P05107	ITB2_HUMAN	ITGB2	Integrin beta-2	0.9945	3.12	2	2	2
						TTEGCLNPR	2	0.9689	1
						VTATECIEQSFVIR	2	0.8237	1
Q515-1	B0QY89	B0QY89_HUMAN	EIF3L	Eukaryotic translation initiation factor 3 subunit L	0.9741	2.31	1	1	3
Q515-2	Q9Y262	EIF3L_HUMAN	EIF3L	Eukaryotic translation initiation factor 3 subunit L	0.9741	2.48	1	1	3
Q515-3	C9JH94	C9JH94_HUMAN	EIF3L	Eukaryotic translation initiation factor 3 subunit L (Fragment)	0.9741	9.33	1	1	3
Q515-4	C9KQ07	C9KQ07_HUMAN	EIF3L	Eukaryotic translation initiation factor 3 subunit L (Fragment)	0.9741	7.65	1	1	3
Q515-5	Q9Y262-2	EIF3L_HUMAN	EIF3L	Isoform 2 of Eukaryotic translation initiation factor 3 subunit L	0.9741	2.71	1	1	3
						VYEIQDIYNSWTK	2	0.9741	3
Q516-1	Q75477	ERLN1_HUMAN	ERLN1	Erlin-1	0.9813	3.47	1	1	2
Q516-2	B0QZ43	B0QZ43_HUMAN	ERLN1	Erlin-1 (Fragment)	0.9813	4.36	1	1	2
Q516-3	O94905	ERLN2_HUMAN	ERLN2	Erlin-2	0.9813	3.54	1	1	2
Q516-4	ESRHW4	ESRHW4_HUMAN	ERLN2	Erlin-2 (Fragment)	0.9813	3.55	1	1	2
						ISEIEDAAFLAR	2	0.9813	2
Q517-1	B0YIW2	B0YIW2_HUMAN	APOC3	Apolipoprotein C-III	0.9819	13.68	1	1	2
Q517-2	P02656	APOC3_HUMAN	APOC3	Apolipoprotein C-III	0.9819	16.16	1	1	2
						DALSSVQESQVAQQAAR	2	0.9819	2
Q518-1	B0YIW6	B0YIW6_HUMAN	ARCN1	Archain 1, isoform CRA_a	0.9849	2.17	1	1	1
Q518-2	P48444	COPD_HUMAN	ARCN1	Coatomer subunit delta	0.9849	2.35	1	1	1
						NSNLEDETLR	2	0.9849	1
Q519-1	B1AH49	B1AH49_HUMAN	MPST	Sulfurtransferase	1.0000	12.95	2	2	6
						AGQPLQLLDASWYLPK	2	0.9996	4
						ALVSAQWVAELR	2	0.9997	2
Q520-1	B1AH78	B1AH78_HUMAN	RAC2	Ras-related C3 botulinum toxin substrate 2 (Fragment)	1.0000	19.88	3	3	6
						CVVVGDAVGK	2	0.9993	4
						SLVSPASYENVR	2	0.9155	1
						YLECSALTQR	2	0.9867	1
Q521-1	B1AHC9	B1AHC9_HUMAN	XRCC6	X-ray repair cross-complementing protein 6	1.0000	5.01	2	2	3
						NIYVLQELDNPQAK	2	0.9997	2
						SDFENPVLQQHFR	2	0.9987	1
Q522-1	B1AHL2	B1AHL2_HUMAN	FBLN1	Fibulin-1	0.9391	1.39	1	1	2
Q522-2	F8W7M9	F8W7M9_HUMAN	FBLN1	Fibulin-1	0.9391	1.42	1	1	2
Q522-3	P23142	FBLN1_HUMAN	FBLN1	Fibulin-1	0.9391	1.42	1	1	2

Q522-4	P23142-2	FBLN1_HUMAN	FBLN1	Isoform A of Fibulin-1	0.9391	1.77	1	1	2
Q522-5	P23142-3	FBLN1_HUMAN	FBLN1	Isoform B of Fibulin-1	0.9391	1.66	1	1	2
Q522-6	P23142-4	FBLN1_HUMAN	FBLN1	Isoform C of Fibulin-1	0.9391	1.46	1	1	2
Q523-1	B1AKG0	B1AKG0_HUMAN	CFHR1	Complement factor H-related protein 1	1.0000	8.86	2	2	3
Q523-2	Q03591	FHR1_HUMAN	CFHR1	Complement factor H-related protein 1	1.0000	7.27	2	2	3
							2	0.9391	2
							2	0.9785	1
Q524-1	B1AKY9	B1AKY9_HUMAN	ATP1A2	Sodium/potassium-transporting ATPase subunit alpha-2	1.0000	2.68	2	2	3
Q524-2	P50993	AT1A2_HUMAN	ATP1A2	Sodium/potassium-transporting ATPase subunit alpha-2	1.0000	2.65	2	2	3
Q524-3	H0Y7C1	H0Y7C1_HUMAN	ATP1A2	Sodium/potassium-transporting ATPase subunit alpha-2 (Fragment)	1.0000	3.78	2	2	3
Q524-4	P13637-2	AT1A3_HUMAN	ATP1A3	Isoform 2 of Sodium/potassium-transporting ATPase subunit alpha-3	1.0000	2.64	2	2	3
Q524-5	P13637-3	AT1A3_HUMAN	ATP1A3	Isoform 3 of Sodium/potassium-transporting ATPase subunit alpha-3	1.0000	2.63	2	2	3
Q524-6	M0R116	M0R116_HUMAN	ATP1A3	Sodium/potassium-transporting ATPase subunit alpha-3	1.0000	2.75	2	2	3
Q524-7	P13637	AT1A3_HUMAN	ATP1A3	Sodium/potassium-transporting ATPase subunit alpha-3	1.0000	2.67	2	2	3
							2	0.9996	2
							2	0.9945	1
Q525-1	Q13310-2	PABP4_HUMAN	PABPC4	Isoform 2 of Polyadenylate-binding protein 4	0.9999	4.44	2	2	3
Q525-2	Q13310-3	PABP4_HUMAN	PABPC4	Isoform 3 of Polyadenylate-binding protein 4	0.9999	4.24	2	2	3
Q525-3	B1ANR0	B1ANR0_HUMAN	PABPC4	Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform 1	0.9999	4.55	2	2	3
Q525-4	Q13310	PABP4_HUMAN	PABPC4	Polyadenylate-binding protein 4	0.9999	4.35	2	2	3
Q525-5	B1ANR1	B1ANR1_HUMAN	PABPC4	Polyadenylate-binding protein 4 (Fragment)	0.9999	21.71	2	2	3
							2	0.9309	2
							2	0.9986	1
Q526-1	B1AP15	B1AP15_HUMAN	CD55	CD55 antigen, decay accelerating factor for complement (Cr1)	0.9991	9.78	2	2	4
Q526-2	B1AP13	B1AP13_HUMAN	CD55	Complement decay-accelerating factor	0.9991	6.98	2	2	4
Q526-3	E9PSH2	E9PSH2_HUMAN	CD55	Complement decay-accelerating factor	0.9991	8.22	2	2	4
Q526-4	H7BY55	H7BY55_HUMAN	CD55	Complement decay-accelerating factor	0.9991	24.03	2	2	4
Q526-5	P08174	DAF_HUMAN	CD55	Complement decay-accelerating factor	0.9991	8.14	2	2	4
Q526-6	H3BLV0	H3BLV0_HUMAN	CD55	Complement decay-accelerating factor (Fragment)	0.9991	9.51	2	2	4
Q526-7	P08174-2	DAF_HUMAN	CD55	Isoform 1 of Complement decay-accelerating factor	0.9991	7.05	2	2	4
Q526-8	P08174-3	DAF_HUMAN	CD55	Isoform 2 of Complement decay-accelerating factor	0.9991	8.07	2	2	4
Q526-9	P08174-4	DAF_HUMAN	CD55	Isoform 3 of Complement decay-accelerating factor	0.9991	8.52	2	2	4
Q526-10	P08174-5	DAF_HUMAN	CD55	Isoform 4 of Complement decay-accelerating factor	0.9991	7.06	2	2	4
Q526-11	P08174-6	DAF_HUMAN	CD55	Isoform 5 of Complement decay-accelerating factor	0.9991	5.9	2	2	4
Q526-12	P08174-7	DAF_HUMAN	CD55	Isoform 6 of Complement decay-accelerating factor	0.9991	5.63	2	2	4
							3	0.994	3
							2	0.8565	1
Q527-1	P07602-2	SAP_HUMAN	PSAP	Isoform Sap-mu-6 of Prosaposin	1.0000	28.71	11	11	23
Q527-2	P07602-3	SAP_HUMAN	PSAP	Isoform Sap-mu-9 of Prosaposin	1.0000	28.65	11	11	23
Q527-3	C9JZ6	C9JZ6_HUMAN	PSAP	Prosaposin	1.0000	28.71	11	11	23
Q527-4	P07602	SAP_HUMAN	PSAP	Prosaposin	1.0000	28.82	11	11	23
Q527-5	B1AVU8	B1AVU8_HUMAN	PSAP	Saposin-D	1.0000	27.01	11	11	23
							2	0.9409	1
							2	0.8363	1
							2	0.8518	1
							2	0.9997	3
							2	0.9996	3
							2	0.9983	4
							2	0.995	3
							2	0.9932	1
							2	0.998	1
							3	0.9996	4
							2	0.9815	1
Q528-1	B3KP96	B3KP96_HUMAN	TRIM16	Tripartite motif-containing protein 16	1.0000	8.76	3	3	5
Q528-2	O95361	TRI16_HUMAN	TRIM16	Tripartite motif-containing protein 16	1.0000	6.74	3	3	5
Q528-3	J3KPT5	J3KPT5_HUMAN	TRIM16L	Tripartite motif-containing protein 16-like protein	1.0000	9.45	3	3	5
							2	0.9994	1
							2	0.9957	2
							2	0.9846	2
Q529-1	B3KPU1	B3KPU1_HUMAN	GNB2	Guanine nucleotide-binding protein G(i1)/G(s)/G(t) subunit beta-1	1.0000	24.58	3	3	5
							3	0.9995	3
							2	0.9995	1
							2	0.9993	1
Q530-1	B3KQ59	B3KQ59_HUMAN	RUVBL2	RuvB-like 2	1.0000	6.94	2	2	3
Q530-2	M0R0Y3	M0R0Y3_HUMAN	RUVBL2	RuvB-like 2	1.0000	8.19	2	2	3
Q530-3	Q9Y230	RUVB2_HUMAN	RUVBL2	RuvB-like 2	1.0000	6.26	2	2	3
							2	0.9987	1
							2	0.9976	2
Q531-1	B3KR41	B3KR41_HUMAN	MAD1L1	Mitotic spindle assembly checkpoint protein MAD1	0.9979	3.99	2	2	4
Q531-2	Q9Y6D9	MD1L1_HUMAN	MAD1L1	Mitotic spindle assembly checkpoint protein MAD1	0.9979	3.48	2	2	4
							2	0.9827	2
							2	0.9247	2
Q532-1	B3KSH1	B3KSH1_HUMAN	EIF3F	Eukaryotic translation initiation factor 3 subunit F	1.0000	11.29	3	3	5
Q532-2	O00303	EIF3F_HUMAN	EIF3F	Eukaryotic translation initiation factor 3 subunit F	1.0000	11.76	3	3	5
							2	0.9969	1
							3	0.9995	2
							3	0.9969	2
Q533-1	P55209-2	NP1L1_HUMAN	NAP1L1	Isoform 2 of Nucleosome assembly protein 1-like 1	1.0000	10.33	3	3	5
Q533-2	B3KV44	B3KV44_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1	1.0000	11.76	3	3	5
Q533-3	B7Z9C2	B7Z9C2_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1	1.0000	10.89	3	3	5
Q533-4	F54H66	F54H66_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1	1.0000	9.92	3	3	5
Q533-5	F8VY59	F8VY59_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1	1.0000	11.62	3	3	5
Q533-6	F8W0I6	F8W0I6_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1	1.0000	10.03	3	3	5
Q533-7	P55209	NP1L1_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1	1.0000	9.72	3	3	5
Q533-8	F8VUX1	F8VUX1_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	16.03	3	3	5
Q533-9	F8VXI6	F8VXI6_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	17.67	3	3	5
Q533-10	F8VY35	F8VY35_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	14.39	3	3	5
Q533-11	F8W0Z0	F8W0Z0_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	18.36	3	3	5
Q533-12	F8W118	F8W118_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	18.18	3	3	5
Q533-13	H0YHC3	H0YHC3_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	19.19	3	3	5
Q533-14	H0YIV4	H0YIV4_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	9.87	3	3	5
							2	0.9994	2
							2	0.9985	2
							2	0.9689	1
Q534-1	B4DD06	B4DD06_HUMAN	DBNL	Drebrin-like protein	1.0000	9.36	2	2	2
Q534-2	B4DDP6	B4DDP6_HUMAN	DBNL	Drebrin-like protein	1.0000	9.95	2	2	2
Q534-3	F8WBG8	F8WBG8_HUMAN	DBNL	Drebrin-like protein	1.0000	29.69	2	2	2
Q534-4	Q9UIU6	DBNL_HUMAN	DBNL	Drebrin-like protein	1.0000	8.84	2	2	2
Q534-5	Q9UIU6-2	DBNL_HUMAN	DBNL	Isoform 2 of Drebrin-like protein	1.0000	8.82	2	2	2
Q534-6	Q9UIU6-3	DBNL_HUMAN	DBNL	Isoform 3 of Drebrin-like protein	1.0000	8.66	2	2	2
							2	0.9978	1
							2	0.9974	1
Q535-1	B4DER1	B4DER1_HUMAN	LARS	Leucine--tRNA ligase, cytoplasmic	1.0000	4.79	4	4	9
Q535-2	B4DJ10	B4DJ10_HUMAN	LARS	Leucine--tRNA ligase, cytoplasmic	1.0000	4.9	4	4	9
Q535-3	F5H698	F5H698_HUMAN	LARS	Leucine--tRNA ligase, cytoplasmic	1.0000	4.87	4	4	9
Q535-4	Q9P2J5	SYLC_HUMAN	LARS	Leucine--tRNA ligase, cytoplasmic	1.0000	4.68	4	4	9
							3	0.9973	3
							2	0.9993	2
							2	0.9268	1
							2	0.9997	3
Q536-1	B4DEW9	B4DEW9_HUMAN	EIF3F	Eukaryotic translation initiation factor 3 subunit F	1.0000	12.98	2	2	3
							2	0.9969	1
							3	0.9995	2
Q537-1	P43034-2	LIS1_HUMAN	PAFAH1B1	Isoform 2 of Platelet-activating factor acetylhydrolase IB subunit alpha	0.9784	7.48	1	1	3
Q537-2	B4DF38	B4DF38_HUMAN	PAFAH1B1	Platelet-activating factor acetylhydrolase IB subunit alpha	0.9784	5.37	1	1	3
Q537-3	P43034	LIS1_HUMAN	PAFAH1B1	Platelet-activating factor acetylhydrolase IB subunit alpha	0.9784	2.68	1	1	3
Q537-4	I3L3N5	I3L3N5_HUMAN	PAFAH1B1	Platelet-activating factor acetylhydrolase IB subunit alpha (Fragment)	0.9784	5.29	1	1	3
							2	0.9784	3
Q538-1	B4DF42	B4DF42_HUMAN	NSF	Vesicle-fusing ATPase	1.0000	13.66	8	10	13
Q538-2	I3L0N3	I3L0N3_HUMAN	NSF	Vesicle-fusing ATPase	1.0000	11.91	8	10	13
Q538-3	P46459	NSF_HUMAN	NSF	Vesicle-fusing ATPase	1.0000	11.83	8	10	13
							2	0.9992	1

						GHQLLSADVDIK	3	0.9946	1
						KAPPQGR	2	0.961	1
						LFGLLVK	2	0.9749	1
						LGANSLGHIIFDEIDAICK	3	0.9995	3
						LLDYVPIGPR	2	0.8999	1
						LQIWHHTAR	2	0.9959	1
						LQIWHHTAR	3	0.9825	1
						NFSGALEGLVR	2	0.9979	1
						YVGSEANIR	2	0.9982	2
Q539-1	B4DFL2	B4DFL2_HUMAN	IDH2	Isocitrate dehydrogenase [NADP]	0.9901	3.25	1	1	1
Q539-2	B4DSZ6	B4DSZ6_HUMAN	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9901	4.04	1	1	1
Q539-3	HOYL11	HOYL11_HUMAN	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9901	4.17	1	1	1
Q539-4	P48735	IDHP_HUMAN	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9901	2.88	1	1	1
Q540-1	B4DGP8	B4DGP8_HUMAN	CANX	Calnexin	1.0000	4.94	2	2	8
Q540-2	P27824	CALX_HUMAN	CANX	Calnexin	1.0000	5.24	2	2	8
						APVPTGEVVFADSFDR	2	0.9997	2
						KIPNPDDFDELEPFR	3	0.9996	6
Q541-1	O94760-2	DDAH1_HUMAN	DDAH1	Isocitrate dehydrogenase [NADP], mitochondrial	1.0000	4.95	1	1	1
Q541-2	B4DGT0	B4DGT0_HUMAN	DDAH1	Isocitrate dehydrogenase [NADP], mitochondrial	1.0000	4.69	1	1	1
Q541-3	B4DYP1	B4DYP1_HUMAN	DDAH1	Isocitrate dehydrogenase [NADP], mitochondrial	1.0000	4.86	1	1	1
Q541-4	O94760	DDAH1_HUMAN	DDAH1	Isocitrate dehydrogenase [NADP], mitochondrial	1.0000	3.16	1	1	1
						EFFVGLSKR	2	0.9614	1
Q542-1	B4DIT7	B4DIT7_HUMAN	TGM2	Protein-glutamine gamma-glutamyltransferase 2	1.0000	9.24	4	4	7
Q542-2	P21980	TGM2_HUMAN	TGM2	Protein-glutamine gamma-glutamyltransferase 2	1.0000	8.15	4	4	7
						ALLVEPVINSYLAER	2	0.9935	1
						RGQPFWLTLHFGR	3	0.9995	2
						SEGTYCCGPVVR	2	0.9988	1
						YLLNLNLEPSEK	2	0.9993	3
Q543-1	B4DK69	B4DK69_HUMAN	AKR1C2	Aldo-keto reductase family 1 member C2	1.0000	16.16	3	3	6
						LNDGHFMPYLGFTYAPAEVK	3	0.9336	1
						QNVQVFEFLTSEEMK	2	0.9997	3
						SIGVSNFNR	2	0.9954	2
Q544-1	B4DKJ3	B4DKJ3_HUMAN	COMP	Cartilage oligomeric matrix protein	1.0000	3.98	2	2	3
Q544-2	G3XAP6	G3XAP6_HUMAN	COMP	Cartilage oligomeric matrix protein	1.0000	3.87	2	2	3
Q544-3	P49747	COMP_HUMAN	COMP	Cartilage oligomeric matrix protein	1.0000	3.7	2	2	3
						DGVGDVCCDDFADAK	2	0.9926	1
						ELQETNAALQDVR	2	0.9995	2
Q545-1	Q15366-2	PCBP2_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	6.56	2	2	3
Q545-2	Q15366-3	PCBP2_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	6.63	2	2	3
Q545-3	Q15366-4	PCBP2_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	7.25	2	2	3
Q545-4	Q15366-5	PCBP2_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	7.16	2	2	3
Q545-5	Q15366-6	PCBP2_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	6.65	2	2	3
Q545-6	Q15366-7	PCBP2_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	7.55	2	2	3
Q545-7	B4DLCO	B4DLCO_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	7.97	2	2	3
Q545-8	B4DXP5	B4DXP5_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	7.45	2	2	3
Q545-9	F8VZX2	F8VZX2_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	7.48	2	2	3
Q545-10	Q15366	PCBP2_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	6.58	2	2	3
Q545-11	F8VXH9	F8VXH9_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	15	2	2	3
Q545-12	F8WOG4	F8WOG4_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	15.19	2	2	3
Q545-13	F8W1G6	F8W1G6_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	11.88	2	2	3
Q545-14	H3BRU6	H3BRU6_HUMAN	PCBP2	Isocitrate dehydrogenase [NADP], mitochondrial	0.9995	7.97	2	2	3
						IITLAGPTNAIFK	2	0.9114	1
						INISEGNCPCR	2	0.9946	2
Q546-1	P62491-2	R811A_HUMAN	RAB11A	Ras-related protein Rab-11A	1.0000	34.19	5	5	8
Q546-2	H3BSC1	H3BSC1_HUMAN	RAB11A	Ras-related protein Rab-11A	1.0000	26.77	5	5	8
Q546-3	J3KQ96	J3KQ96_HUMAN	RAB11A	Ras-related protein Rab-11A	1.0000	34.19	5	5	8
Q546-4	P62491	R811A_HUMAN	RAB11A	Ras-related protein Rab-11A	1.0000	24.54	5	5	8
Q546-5	H3BMH2	H3BMH2_HUMAN	RAB11A	Ras-related protein Rab-11A (Fragment)	1.0000	34.19	5	5	8
Q546-6	B4DMK0	B4DMK0_HUMAN	RAB11B	Ras-related protein Rab-11B	1.0000	29.61	5	5	8
Q546-7	Q15907	R811B_HUMAN	RAB11B	Ras-related protein Rab-11B	1.0000	24.31	5	5	8
						AQIWDTAGQER	2	0.9969	1
						GAVGALLYVDIAK	2	0.9992	2
						NEFNLESK	2	0.9217	1
						STIGVEFATR	2	0.9985	3
						VVLIGDSGVGK	2	0.9982	1
Q547-1	B4DN89	B4DN89_HUMAN	SFRS2	Serine/arginine-rich splicing factor 2	0.9991	11.96	2	2	2
Q547-2	Q01130	SRSF2_HUMAN	SRSF2	Serine/arginine-rich splicing factor 2	0.9991	11.31	2	2	2
Q547-3	J3KP15	J3KP15_HUMAN	SRSF2	Serine/arginine-rich splicing factor 2 (Fragment)	0.9991	18.8	2	2	2
Q547-4	J3QL05	J3QL05_HUMAN	SRSF2	Serine/arginine-rich splicing factor 2 (Fragment)	0.9991	19.23	2	2	2
						DAEDAMDQDGAVIDGR	2	0.9721	1
						VGDVYIPR	2	0.9789	1
Q548-1	B4DNW0	B4DNW0_HUMAN	ACY1	Aminoacylase-1	1.0000	13.45	4	5	9
Q548-2	F8WC59	F8WC59_HUMAN	ACY1	Aminoacylase-1	1.0000	33.33	4	5	9
Q548-3	Q03154	ACY1_HUMAN	ACY1	Aminoacylase-1	1.0000	16.42	4	5	9
Q548-4	C9Y20	C9Y20_HUMAN	ACY1	Aminoacylase-1 (Fragment)	1.0000	29.39	4	5	9
Q548-5	Q03154-3	ACY1_HUMAN	ACY1	Aminoacylase-1	1.0000	19.53	4	5	9
						AGFALDEGIANPTDAFTVYSER	2	0.9997	2
						AGFALDEGIANPTDAFTVYSER	3	0.8982	1
						CVSIQYLEAVR	2	0.9892	2
						GPEEHPSVTLR	3	0.8485	1
Q549-1	B4DPJ8	B4DPJ8_HUMAN	CCT6A	T-complex protein 1 subunit zeta	1.0000	15.8	5	5	9
						AQLGVAFADALLIPK	2	0.9996	3
						GIDPFLDALSK	2	0.9945	1
						QADLYISEGLHPR	3	0.9927	1
						VHAEADVLTEAVDSILAIAK	3	0.9967	1
						VLAQNSGFDLQETLVK	2	0.9997	3
Q550-1	B4DQI4	B4DQI4_HUMAN	ABHD14B	Alpha/beta hydrolase domain-containing protein 14B	1.0000	32.45	6	7	12
Q550-2	Q361U4	ABHEB_HUMAN	ABHD14B	Alpha/beta hydrolase domain-containing protein 14B	1.0000	29.05	6	7	12
						AVAILDPLGLGHSK	3	0.9055	1
						EALPGSGOAR	2	0.9926	1
						EGTIQVGGQALFFR	2	0.9994	4
						FSSETWQNLGTLHR	2	0.9797	1
						FSVLLHGIR	2	0.9996	2
						FSVLLHGIR	3	0.9984	2
						SVLLHGIR	2	0.888	1
Q551-1	Q13595-2	TRA2A_HUMAN	TRA2A	Transformer-2 protein homolog alpha	1.0000	20.35	2	2	2
Q551-2	B4DQI6	B4DQI6_HUMAN	TRA2A	Transformer-2 protein homolog alpha	1.0000	12.78	2	2	2
Q551-3	B4DU9A	B4DU9A_HUMAN	TRA2A	Transformer-2 protein homolog alpha	1.0000	12.71	2	2	2
Q551-4	Q13595	TRA2A_HUMAN	TRA2A	Transformer-2 protein homolog alpha	1.0000	8.16	2	2	2
						GFAFVYFER	2	0.9996	1
						YGPLSGVNVVDQDR	2	0.9922	1
Q552-1	B4DQJ8	B4DQJ8_HUMAN	PGD	6-phosphogluconate dehydrogenase, decarboxylating	1.0000	7.87	3	3	5
Q552-2	P52209	6PGD_HUMAN	PGD	6-phosphogluconate dehydrogenase, decarboxylating	1.0000	7.66	3	3	5
Q552-3	F5H7U0	F5H7U0_HUMAN	PGD	Uncharacterized protein	1.0000	8.03	3	3	5
						GLIFVSGVSGGEEGAR	2	0.9993	2
						ISVYAGGFMALLR	2	0.9993	2
						SFLEDIRK	2	0.9487	1
Q553-1	B4DQV7	B4DQV7_HUMAN	NPC2	Epididymal secretory protein E1	0.9844	12.8	1	1	3
Q553-2	E7EMS2	E7EMS2_HUMAN	NPC2	Epididymal secretory protein E1	0.9844	7.96	1	1	3
Q553-3	G3V3E8	G3V3E8_HUMAN	NPC2	Epididymal secretory protein E1	0.9844	9.2	1	1	3
Q553-4	J3KMV5	J3KMV5_HUMAN	NPC2	Epididymal secretory protein E1	0.9844	10.81	1	1	3
Q553-5	P61916	NPC2_HUMAN	NPC2	Epididymal secretory protein E1	0.9844	10.6	1	1	3
Q553-6	G3V2V8	G3V2V8_HUMAN	NPC2	Epididymal secretory protein E1 (Fragment)	0.9844	13.11	1	1	3
Q553-7	G3V3D1	G3V3D1_HUMAN	NPC2	Epididymal secretory protein E1 (Fragment)	0.9844	7.24	1	1	3
Q553-8	HOYI21	HOYI21_HUMAN	NPC2	Epididymal secretory protein E1 (Fragment)	0.9844	9.25	1	1	3
						EVNVSPCPTQPCQLSK	2	0.9844	3
Q554-1	B4DQW8	B4DQW8_HUMAN	ANKS1A	Ankyrin repeat and SAM domain-containing protein 1A	0.9819	13.44	1	1	1
Q554-2	Q92625	ANKS1A_HUMAN	ANKS1A	Ankyrin repeat and SAM domain-containing protein 1A	0.9819	3.79	1	1	1
						RLSSGFGGGGGGGGGGGGGGGGGGGGGSSSHPLSLLSMMWR	3	0.9736	1
Q555-1	P57053	H2BFS_HUMAN	H2BFS	Histone H2B type F-S	1.0000	26.98	7	7	11
Q555-2	P62807	H2B1C_HUMAN	HIST1H2BC	Histone H2B type 1-C/E/F/G/I	1.0000	26.98	7	7	11

Q555-3	P58876	H2B1D_HUMAN	HIST1H2BD	Histone H2B type 1-D	1.0000	26.98	7	7	11
Q555-4	Q93079	H2B1H_HUMAN	HIST1H2BH	Histone H2B type 1-H	1.0000	26.98	7	7	11
Q555-5	Q60814	H2B1K_HUMAN	HIST1H2BK	Histone H2B type 1-K	1.0000	26.98	7	7	11
Q555-6	Q99880	H2B1L_HUMAN	HIST1H2BL	Histone H2B type 1-L	1.0000	26.98	7	7	11
Q555-7	Q99879	H2B1M_HUMAN	HIST1H2BM	Histone H2B type 1-M	1.0000	26.98	7	7	11
Q555-8	U3KQK0	U3KQK0_HUMAN	HIST1H2BN	Histone H2B	1.0000	20.48	7	7	11
Q555-9	Q99877	H2B1N_HUMAN	HIST1H2BN	Histone H2B type 1-N	1.0000	26.98	7	7	11
Q555-10	B4DR52	B4DR52_HUMAN	HIST2H2BF	Histone H2B	1.0000	20.48	7	7	11
Q555-11	Q5QNW6	H2B2F_HUMAN	HIST2H2BF	Histone H2B type 2-F	1.0000	26.98	7	7	11
Q555-12	Q5QNW6-2	H2B2F_HUMAN	HIST2H2BF	Isoform 2 of Histone H2B type 2-F	1.0000	25.37	7	7	11
				AMGIMSVFNDIFER		2	0.9995	4	
				ESYSVYVYK		2	0.8252	1	
				KEYSVYVYK		2	0.941	1	
				LLPGELAK		2	0.9986	2	
				MNSFVNDIFER		2	0.8689	1	
				NSFVNDIFER		2	0.814	1	
				SFVNDIFER		2	0.9578	1	
Q556-1	B4DR63	B4DR63_HUMAN	PSMC1	26S protease regulatory subunit 4	0.9999	12.26	3	3	3
Q556-2	P62191	PR54_HUMAN	PSMC1	26S protease regulatory subunit 4	0.9999	10.73	3	3	3
				AICTAGIALMAR		2	0.9167	1	
				AVANQTSATFLR		2	0.9637	1	
				VAEEHAPSIVHDEIDAIGTK		3	0.9982	1	
Q557-1	Q9Y6E0-2	STK24_HUMAN	STK24	Isoform A of Serine/threonine-protein kinase 24	1.0000	28.07	8	9	17
Q557-2	Q9Y6E0	STK24_HUMAN	STK24	Serine/threonine-protein kinase 24	1.0000	27.31	8	9	17
Q557-3	B4DR80	B4DR80_HUMAN	STK24	Serine/threonine-protein kinase 24 12 kDa subunit	1.0000	29.37	8	9	17
				AANVLSEHGEVK		2	0.9963	1	
				ADIWSLGITAEIAR		2	0.9997	3	
				ADIWSLGITAEIAR		3	0.9996	2	
				GAIVLAEEACPGISDTMVAQLVQR		3	0.9952	2	
				LADFGVAGQLTDTQIKR		3	0.9532	1	
				RPSQCLSTISPLFAELK		3	0.9948	3	
				SQACGGNLSGSEELR		2	0.9997	3	
				VSFLPK		2	0.9889	1	
				YSLSGGTSSTH		2	0.9992	1	
Q558-1	B4DT28	B4DT28_HUMAN	HNRNPR	Heterogeneous nuclear ribonucleoprotein R	0.9051	2.63	1	1	1
Q558-2	E7ETM7	E7ETM7_HUMAN	HNRNPR	Heterogeneous nuclear ribonucleoprotein R	0.9051	2.75	1	1	1
Q558-3	O43390	HNRNPR_HUMAN	HNRNPR	Heterogeneous nuclear ribonucleoprotein R	0.9051	2.05	1	1	1
Q558-4	O43390-2	HNRNPR_HUMAN	HNRNPR	Isoform 2 of Heterogeneous nuclear ribonucleoprotein R	0.9051	2.04	1	1	1
Q558-5	O43390-3	HNRNPR_HUMAN	HNRNPR	Isoform 3 of Heterogeneous nuclear ribonucleoprotein R	0.9051	2.18	1	1	1
Q558-6	O43390-4	HNRNPR_HUMAN	HNRNPR	Isoform 4 of Heterogeneous nuclear ribonucleoprotein R	0.9051	2.43	1	1	1
				NLATTVTIEILEK		2	0.9051	1	
Q559-1	B4DTC3	B4DTC3_HUMAN	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0	0.9333	2.64	1	1	1
Q559-2	Q14103	HNRNPD_HUMAN	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0	0.9333	2.25	1	1	1
Q559-3	D6RAF8	D6RAF8_HUMAN	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	0.9333	3.62	1	1	1
Q559-4	D6RAC9	D6RAC9_HUMAN	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	0.9333	5.16	1	1	1
Q559-5	D6RF44	D6RF44_HUMAN	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	0.9333	7.21	1	1	1
Q559-6	HOY8G5	HOY8G5_HUMAN	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	0.9333	3.08	1	1	1
Q559-7	HOYA96	HOYA96_HUMAN	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0 (Fragment)	0.9333	3.81	1	1	1
Q559-8	Q14103-2	HNRNPD_HUMAN	HNRNPD	Isoform 2 of Heterogeneous nuclear ribonucleoprotein D0	0.9333	2.38	1	1	1
Q559-9	Q14103-3	HNRNPD_HUMAN	HNRNPD	Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0	0.9333	2.61	1	1	1
Q559-10	Q14103-4	HNRNPD_HUMAN	HNRNPD	Isoform 4 of Heterogeneous nuclear ribonucleoprotein D0	0.9333	2.79	1	1	1
Q559-11	O14979	HNRNPD_HUMAN	HNRNPD	Heterogeneous nuclear ribonucleoprotein D-like	0.9333	1.9	1	1	1
Q559-12	O14979-2	HNRNPD_HUMAN	HNRNPD	Isoform 2 of Heterogeneous nuclear ribonucleoprotein D-like	0.9333	2.66	1	1	1
Q559-13	O14979-3	HNRNPD_HUMAN	HNRNPD	Isoform 3 of Heterogeneous nuclear ribonucleoprotein D-like	0.9333	3.28	1	1	1
				GGFVFLK		2	0.9333	1	
Q560-1	B4DTG2	B4DTG2_HUMAN	EEF1G	Elongation factor 1-gamma	1.0000	14.78	6	7	11
Q560-2	P26641	EEF1G_HUMAN	EEF1G	Elongation factor 1-gamma	1.0000	16.48	6	7	11
				EYFSWIGAFQHVSK		2	0.9956	2	
				GGELAFPLSPDWQVDYESTWR		2	0.9594	1	
				GGELAFPLSPDWQVDYESTWR		3	0.9128	1	
				ILGLDAYLK		2	0.9957	2	
				KLDGSEETQTLVR		2	0.9991	2	
				LDPGSEETQTLVR		2	0.997	2	
				WFLTCINQPKR		2	0.9799	1	
Q561-1	P49368-2	TCPG_HUMAN	CTT3	Isoform 2 of T-complex protein 1 subunit gamma	1.0000	13.21	6	6	9
Q561-2	B4DUR8	B4DUR8_HUMAN	CTT3	T-complex protein 1 subunit gamma	1.0000	13.4	6	6	9
Q561-3	P49368	TCPG_HUMAN	CTT3	T-complex protein 1 subunit gamma	1.0000	12.29	6	6	9
				ELGIWEPLAVK		2	0.9965	1	
				DDIVSGHK		2	0.9978	2	
				NLQDSLEK		2	0.9251	1	
				NLQDAMQVCR		2	0.9889	1	
				TLQNCAGSTIR		2	0.9988	2	
				WSSLACNIALDAVK		2	0.9994	2	
Q562-1	J3QTR3	J3QTR3_HUMAN	RPS27A	Ubiquitin (Fragment)	1.0000	37.74	4	4	15
Q562-2	P62979	RS27A_HUMAN	RPS27A	Ubiquitin-40S ribosomal protein S27a	1.0000	25.64	4	4	15
Q562-3	P62987	RL40_HUMAN	UBA52	Ubiquitin-60S ribosomal protein L40	1.0000	31.25	4	4	15
Q562-4	POCG47	UBB_HUMAN	UBB	Polyubiquitin-B	1.0000	17.47	4	4	15
Q562-5	B4DV12	B4DV12_HUMAN	UBB	Ubiquitin	1.0000	26.14	4	4	15
Q562-6	J3QKN0	J3QKN0_HUMAN	UBB	Ubiquitin (Fragment)	1.0000	19.42	4	4	15
Q562-7	J3Q539	J3Q539_HUMAN	UBB	Ubiquitin (Fragment)	1.0000	43.01	4	4	15
Q562-8	J3QLP7	J3QLP7_HUMAN	UBBP4	Protein UBBP4	1.0000	17.86	4	4	15
Q562-9	J3QRK5	J3QRK5_HUMAN	UBBP4	Protein UBBP4	1.0000	17.47	4	4	15
Q562-10	F5H041	F5H041_HUMAN	UBC	Polyubiquitin-C	1.0000	6.57	4	4	15
Q562-11	POCG48	UBC_HUMAN	UBC	Polyubiquitin-C	1.0000	5.84	4	4	15
Q562-12	Q96C32	Q96C32_HUMAN	UBC	Polyubiquitin-C	1.0000	13.11	4	4	15
Q562-13	F5GK77	F5GK77_HUMAN	UBC	Polyubiquitin-C (Fragment)	1.0000	23.67	4	4	15
Q562-14	F5GYU3	F5GYU3_HUMAN	UBC	Polyubiquitin-C (Fragment)	1.0000	29.85	4	4	15
Q562-15	F5H265	F5H265_HUMAN	UBC	Polyubiquitin-C (Fragment)	1.0000	26.85	4	4	15
Q562-16	F5H223	F5H223_HUMAN	UBC	Polyubiquitin-C (Fragment)	1.0000	29.41	4	4	15
Q562-17	F5H388	F5H388_HUMAN	UBC	Polyubiquitin-C (Fragment)	1.0000	25.81	4	4	15
Q562-18	F5H6Q2	F5H6Q2_HUMAN	UBC	Polyubiquitin-C (Fragment)	1.0000	32.79	4	4	15
Q562-19	F5H747	F5H747_HUMAN	UBC	Polyubiquitin-C (Fragment)	1.0000	25	4	4	15
				ESTLHLVLR		2	0.9996	1	
				IQDREGIPPOQR		2	0.9994	10	
				TITLEVPSDTIENVK		2	0.9996	3	
				TITLEVPSDTIENVKAK		2	0.9915	1	
Q563-1	B4DVY1	B4DVY1_HUMAN	EIF3D	Eukaryotic translation initiation factor 3 subunit D	1.0000	13.83	6	7	11
Q563-2	O15371	EIF3D_HUMAN	EIF3D	Eukaryotic translation initiation factor 3 subunit D	1.0000	12.59	6	7	11
				IFHTVTTTDDPVIR		3	0.9841	1	
				LGDDIDILVR		2	0.9996	1	
				NLAMEATYINHNFSQQCLR		3	0.8839	1	
				SVYSWDIVVQR		2	0.9996	2	
				VADWTGATYQDKR		2	0.9995	2	
				WKLGGDIDILVR		2	0.9209	1	
				WKLGGDIDILVR		3	0.9971	3	
Q564-1	B4DXW1	B4DXW1_HUMAN	ACTR3	Actin-related protein 3	1.0000	5.72	2	2	3
Q564-2	F5H3P5	F5H3P5_HUMAN	ACTR3	Actin-related protein 3	1.0000	5.9	2	2	3
				DTYFIQQLLR		2	0.9994	2	
				YSYVCPDLVK		2	0.9973	1	
Q565-1	O15523	DDX3Y_HUMAN	DDX3Y	ATP-dependent RNA helicase DDX3Y	1.0000	2.73	2	2	2
Q565-2	B4DXX7	B4DXX7_HUMAN	DDX3Y	Uncharacterized protein	1.0000	2.74	2	2	2
				GCHLLVATPGR		2	0.999	1	
				HAIPKIK		2	0.9983	1	
Q566-1	B4DXY7	B4DXY7_HUMAN	ALDH9A1	4-trimethylaminobutylaldehyde dehydrogenase	0.9981	5.9	2	2	2
Q566-2	P49189	ALDH9A1_HUMAN	ALDH9A1	4-trimethylaminobutylaldehyde dehydrogenase	0.9981	5.06	2	2	2
				ANDITFGLAAGVFTR		2	0.9179	1	
				VTIEYSQKL		2	0.9769	1	
Q567-1	B4DY08	B4DY08_HUMAN	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	1.0000	20.49	6	6	10
Q567-2	G3VZD1	G3VZD1_HUMAN	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	1.0000	19.34	6	6	10
Q567-3	G3VAC1	G3VAC1_HUMAN	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	1.0000	20.21	6	6	10
Q567-4	G3V576	G3V576_HUMAN	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	1.0000	25.54	6	6	10
Q567-5	P07910	HNRNPC_HUMAN	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	1.0000	19.28	6	6	10
Q567-6	G3V4W0	G3V4W0_HUMAN	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment)	1.0000	22.52	6	6	10

Q567-7	P07910-2	HNRPC_HUMAN	HNRNPC	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/	1.0000	20.14	6	6	10
						GDDLQAIKK	2	0.9771	1
						GFAFVQYVNER	2	0.9996	2
						LKGDDLQAIKK	2	0.9865	1
						MIAGQVLDINLAAEPK	2	0.9994	3
						SDVEAIFSK	2	0.9715	1
						VFIGNLNLTIVVK	2	0.9994	2
Q568-1	B4DZB8	B4DZB8_HUMAN	COPB2	Coatamer protein complex, subunit beta 2 (Beta prime), isofo	1.0000	5.47	4	4	6
Q568-2	P35606	COPB2_HUMAN	COPB2	Coatamer subunit beta'	1.0000	5.3	4	4	6
						EAFVVEWVK	2	0.9635	1
						GSNNVALYDEGSIIVK	2	0.9989	1
						LESTLNYGMER	2	0.9968	2
						TFEVCDLPVR	2	0.998	2
Q569-1	P29401-2	TKT_HUMAN	TKT	Isoform 2 of Transketolase	1.0000	22.19	9	10	27
Q569-2	B4E022	B4E022_HUMAN	TKT	Transketolase	1.0000	24.31	9	10	27
Q569-3	P29401	TKT_HUMAN	TKT	Transketolase	1.0000	22.47	9	10	27
						AVWAEAGFLAEAEELLNLR	2	0.9946	3
						AVWAEAGFLAEAEELLNLR	3	0.9835	4
						CEAFGWHAIVDGHVSVEELCK	3	0.9978	3
						ILTVEDHMYEGGGEAV	2	0.8575	1
						LDNLVAILDINR	2	0.9993	5
						SGKPAELLK	2	0.9967	2
						SKDDQVTIVIGAGVTLHEALAAELKK	4	0.9351	1
						STFAAFFTR	2	0.8236	1
						TSRPENAIYNNNEDFVGQAK	3	0.9979	3
						TVPCSTFAAFFTR	2	0.9995	4
Q570-1	Q9P289-2	MST4_HUMAN	MST4	Isoform 2 of Serine/threonine-protein kinase MST4	1.0000	6.49	2	2	2
Q570-2	B4E0Y9	B4E0Y9_HUMAN	MST4	Serine/threonine-protein kinase MST4	1.0000	5.02	2	2	2
Q570-3	Q8NB1	Q8NB1_HUMAN	MST4	Serine/threonine-protein kinase MST4	1.0000	5.61	2	2	2
Q570-4	Q9P289	MST4_HUMAN	MST4	Serine/threonine-protein kinase MST4	1.0000	5.29	2	2	2
Q570-5	O00506-2	STK25_HUMAN	STK25	Isoform 2 of Serine/threonine-protein kinase 25	1.0000	6.3	2	2	2
Q570-6	O00506-3	STK25_HUMAN	STK25	Isoform 3 of Serine/threonine-protein kinase 25	1.0000	6.63	2	2	2
Q570-7	O00506	STK25_HUMAN	STK25	Serine/threonine-protein kinase 25	1.0000	5.16	2	2	2
Q570-8	C9J232	C9J232_HUMAN	STK25	Serine/threonine-protein kinase 25 (Fragment)	1.0000	12.43	2	2	2
Q570-9	C9J6L2	C9J6L2_HUMAN	STK25	Serine/threonine-protein kinase 25 (Fragment)	1.0000	13.66	2	2	2
Q570-10	C9JCC0	C9JCC0_HUMAN	STK25	Serine/threonine-protein kinase 25 (Fragment)	1.0000	13.5	2	2	2
Q570-11	C9JDH9	C9JDH9_HUMAN	STK25	Serine/threonine-protein kinase 25 (Fragment)	1.0000	14.86	2	2	2
Q570-12	H7C279	H7C279_HUMAN	STK25	Serine/threonine-protein kinase 25 (Fragment)	1.0000	8.91	2	2	2
						ADIWSLGITAEI LAK	2	0.9973	1
						VLFLIPK	2	0.9889	1
Q571-1	B4E1F0	B4E1F0_HUMAN	SERPING1	Plasma protease C1 inhibitor	1.0000	22.18	12	13	29
Q571-2	B4E1H2	B4E1H2_HUMAN	SERPING1	Plasma protease C1 inhibitor	1.0000	25	12	13	29
Q571-3	P05155	IC1_HUMAN	SERPING1	Plasma protease C1 inhibitor	1.0000	22.4	12	13	29
						DFTCVHQAIK	2	0.9995	1
						FQPTLLTLP	2	0.9458	1
						GVTSVSQIFHSPDLAIR	2	0.9997	3
						GVTSVSQIFHSPDLAIR	3	0.995	1
						HRLEDMEQALSPSVFK	3	0.9135	1
						LLDSPSDTR	2	0.9988	4
						LVLINAYLSAK	2	0.9996	3
						TLLVFEVQPPF	2	0.9254	1
						TLLVFEVQPPFL	2	0.9916	2
						TLLVFEVQPPFLF	2	0.9859	3
						TNLESLSYPK	2	0.9995	4
						TNLESLSYPKDFTCVHQALK	3	0.9887	2
						VITSQDMLSIMEX	2	0.9994	3
Q572-1	Q02241-2	KIF23_HUMAN	KIF23	Isoform 2 of Kinesin-like protein KIF23	0.9064	2.34	1	1	2
Q572-2	B4E1K0	B4E1K0_HUMAN	KIF23	Kinesin-like protein KIF23	0.9064	2.97	1	1	2
Q572-3	H7BYN4	H7BYN4_HUMAN	KIF23	Kinesin-like protein KIF23	0.9064	2.1	1	1	2
Q572-4	Q02241	KIF23_HUMAN	KIF23	Kinesin-like protein KIF23	0.9064	2.08	1	1	2
						MIVCVNPKAEDYEENLQVMR	2	0.9064	2
Q573-1	B4E1Z4	B4E1Z4_HUMAN	CFB	Complement factor B	1.0000	34.83	40	44	91
						AHCPRPHDFENGGEYWPR	2	0.9986	1
						AHCPRPHDFENGGEYWPR	3	0.9985	4
						AHCPRPHDFENGGEYWPR	4	0.9981	2
						ALFVSEEEK	2	0.9972	2
						ALFVSEEEK	2	0.9993	2
						ALRLPTTTCCQQKEELLPAQDIK	3	0.9992	3
						ARPGSCSLEGVEIK	2	0.9387	2
						AVISRGPDVFAK	2	0.9893	2
						CLPCTEGTTR	2	0.8794	1
						CLVNLIEK	2	0.9935	2
						CSSNLVLGTSSER	2	0.9988	3
						DAQYAPGYDKVK	2	0.9964	3
						DFHINLFQVLPWLK	3	0.9971	1
						DISEVTPR	2	0.9996	2
						DLEIEVLFHPNY	2	0.8443	1
						DLLYGKDR	2	0.9977	2
						DNEQHVFK	2	0.9854	1
						EAGIPFEDYDVALIK	2	0.9997	5
						EAGIPFEDYDVALIK	3	0.9453	1
						EDYLDVYVFGVGPLVNQVNNALASK	3	0.9862	2
						EDYLDVYVFGVGPLVNQVNNALASK	3	0.9979	2
						FIVQGVISWGVVDCK	2	0.8418	1
						FLCTGGVSPYADPNTCR	2	0.9997	3
						GDSGGPLIVHK	2	0.9989	2
						GDSGGPLIVHKR	2	0.9995	4
						GLVTYATPK	2	0.9551	1
						HAFILDQTK	2	0.9986	3
						HAILLTDGK	2	0.9971	1
						KNQGILEFYGDIALLK	3	0.9966	2
						LEDSVTHCSR	2	0.9996	3
						LLGMETMAWQEIR	2	0.9996	2
						LLQEGQALEYVCPGPPVPVQTR	3	0.9996	2
						NDRIDYAGVKG	2	0.9944	1
						NPREDYLDVYVFGVGPLVNQVNNALASK	3	0.9975	2
						QLNEINYEDHK	2	0.9988	1
						QLNEINYEDHKLK	2	0.9609	2
						SLARPQGSCLSEGVEIK	3	0.912	1
						SSGQWQTPGATR	2	0.9516	1
						STGWSWLK	2	0.9813	1
						VASYGVKPR	2	0.9997	1
						VSEADSSNADWVTK	2	0.9997	4
						YGLVTYATPK	2	0.9997	4
						YQGTIRPICLPCTEGTTR	2	0.9993	3
						YQGTIRPICLPCTEGTTR	3	0.9993	2
Q574-1	P84103	SRSF3_HUMAN	SRSF3	Serine/arginine-rich splicing factor 3	1.0000	23.17	4	5	12
Q574-2	B4E241	B4E241_HUMAN	SRSF3	Serine/arginine-rich splicing factor 3	1.0000	30.65	4	5	12
						AFGYGQPR	2	0.9997	3
						DSCPLDCK	2	0.9938	1
						NPPGFAFVEFEDPR	2	0.9997	3
						NPPGFAFVEFEDPR	3	0.9993	2
						NPPGFAFVEFEDPRDAADAVR	3	0.9981	3
Q575-1	O75487	GPC4_HUMAN	GPC4	Glypican-4	0.9999	14.21	5	5	5
Q575-2	B4E2C0	B4E2C0_HUMAN	GPC4	Secreted glypican-4	0.9999	16.26	5	5	5
						KFWSSLPSNVCNDR	3	0.9131	1
						LEGPFNIESVMDPIDVK	2	0.9897	1
						VFGCGGPKPLPAG	2	0.8852	1
						VFGCGGPKPLPAGR	2	0.9944	1
						YLFVAVTNGLANQGNHREYQVDTSPDILILR	3	0.8767	1
Q576-1	B4E2Q4	B4E2Q4_HUMAN	EIF3M	Eukaryotic translation initiation factor 3 subunit M	0.9428	4.96	1	1	1
Q576-2	Q7L2H7	EIF3M_HUMAN	EIF3M	Eukaryotic translation initiation factor 3 subunit M	0.9428	3.21	1	1	1
Q576-3	HOYQ8	HOYQ8_HUMAN	EIF3M	Eukaryotic translation initiation factor 3 subunit M (Fragmen	0.9428	5.45	1	1	1

						LTTFMGMAVENK	2	0.9428	1
Q577-1	B4E363	B4E363_HUMAN	FARSA	Phenylalanine--tRNA ligase alpha subunit	1.0000	2.94	1	2	5
Q577-2	K7ER00	K7ER00_HUMAN	FARSA	Phenylalanine--tRNA ligase alpha subunit	1.0000	2.55	1	2	5
Q577-3	K7ER16	K7ER16_HUMAN	FARSA	Phenylalanine--tRNA ligase alpha subunit	1.0000	5.96	1	2	5
Q577-4	Q9Y285	SYFA_HUMAN	FARSA	Phenylalanine--tRNA ligase alpha subunit	1.0000	2.76	1	2	5
Q577-5	K7EK06	K7EK06_HUMAN	FARSA	Phenylalanine--tRNA ligase alpha subunit (Fragment)	1.0000	8.33	1	2	5
						SLOALGEVIEAELR	2	0.9996	3
						SLOALGEVIEAELR	2	0.9991	2
Q578-1	B5M8Z0	B5M8Z0_HUMAN	EML4	Echinoderm microtubule-associated protein-like 4	0.9999	1.71	2	2	3
Q578-2	Q9HC35	EMAL4_HUMAN	EML4	Echinoderm microtubule-associated protein-like 4	0.9999	1.73	2	2	3
Q578-3	Q9HC35-2	EMAL4_HUMAN	EML4	Isoform 2 of Echinoderm microtubule-associated protein-like 4	0.9999	1.84	2	2	3
						AALADVLR	2	0.9867	1
						WFLVDAETR	2	0.9937	2
Q579-1	Q15435-2	PP1R7_HUMAN	PPP1R7	Isoform 2 of Protein phosphatase 1 regulatory subunit 7	0.9489	3.47	1	1	1
Q579-2	Q15435-3	PP1R7_HUMAN	PPP1R7	Isoform 3 of Protein phosphatase 1 regulatory subunit 7	0.9489	3.93	1	1	1
Q579-3	Q15435-4	PP1R7_HUMAN	PPP1R7	Isoform 4 of Protein phosphatase 1 regulatory subunit 7	0.9489	4.64	1	1	1
Q579-4	B5M8Z8	B5M8Z8_HUMAN	PPP1R7	Protein phosphatase 1 regulatory subunit 7	0.9489	4.01	1	1	1
Q579-5	B5MCY6	B5MCY6_HUMAN	PPP1R7	Protein phosphatase 1 regulatory subunit 7	0.9489	4.98	1	1	1
Q579-6	Q15435	PP1R7_HUMAN	PPP1R7	Protein phosphatase 1 regulatory subunit 7	0.9489	3.06	1	1	1
Q579-7	C9I177	C9I177_HUMAN	PPP1R7	Protein phosphatase 1 regulatory subunit 7 (Fragment)	0.9489	3.81	1	1	1
Q579-8	C9I073	C9I073_HUMAN	PPP1R7	Protein phosphatase 1 regulatory subunit 7 (Fragment)	0.9489	3.9	1	1	1
Q579-9	H7C003	H7C003_HUMAN	PPP1R7	Protein phosphatase 1 regulatory subunit 7 (Fragment)	0.9489	3.28	1	1	1
						IEGLQNLVNL	2	0.9489	1
Q580-1	B5MC07	B5MC07_HUMAN	AGR2	Anterior gradient protein 2 homolog	1.0000	24.47	4	6	11
Q580-2	C9J3E2	C9J3E2_HUMAN	AGR2	Anterior gradient protein 2 homolog (Fragment)	1.0000	35.11	4	6	11
						GWGDQLWTQTYYEALYK	2	0.9997	3
						HLSPDGGQVPR	2	0.9917	1
						LAEQFVLLNLVYETDK	2	0.9997	3
						LAEQFVLLNLVYETDK	3	0.9995	2
						LAEQFVLLNLVYETDKHLSPDGGQVPR	3	0.9737	1
						LAEQFVLLNLVYETDKHLSPDGGQVPR	4	0.987	1
Q581-1	P22309-2	UD11_HUMAN	UGT1A1	Isoform 2 of UDP-glucuronosyltransferase 1-1	1.0000	4.73	1	1	2
Q581-2	P22309	UD11_HUMAN	UGT1A1	UDP-glucuronosyltransferase 1-1	1.0000	3.94	1	1	2
Q581-3	Q9HAW8-2	UD110_HUMAN	UGT1A10	Isoform 2 of UDP-glucuronosyltransferase 1-10	1.0000	4.76	1	1	2
Q581-4	Q9HAW8	UD110_HUMAN	UGT1A10	UDP-glucuronosyltransferase 1-10	1.0000	3.96	1	1	2
Q581-5	P35503-3	UD13_HUMAN	UGT1A3	Isoform 2 of UDP-glucuronosyltransferase 1-3	1.0000	4.72	1	1	2
Q581-6	P35503	UD13_HUMAN	UGT1A3	UDP-glucuronosyltransferase 1-3	1.0000	3.93	1	1	2
Q581-7	P22310-2	UD14_HUMAN	UGT1A4	Isoform 2 of UDP-glucuronosyltransferase 1-4	1.0000	4.72	1	1	2
Q581-8	P22310	UD14_HUMAN	UGT1A4	UDP-glucuronosyltransferase 1-4	1.0000	3.93	1	1	2
Q581-9	P35504-2	UD15_HUMAN	UGT1A5	Isoform 2 of UDP-glucuronosyltransferase 1-5	1.0000	4.72	1	1	2
Q581-10	P35504	UD15_HUMAN	UGT1A5	UDP-glucuronosyltransferase 1-5	1.0000	3.93	1	1	2
Q581-11	P19224-2	UD16_HUMAN	UGT1A6	Isoform 2 of UDP-glucuronosyltransferase 1-6	1.0000	7.92	1	1	2
Q581-12	B5MCT4	B5MCT4_HUMAN	UGT1A6	UDP-glucuronosyltransferase 1-6	1.0000	11.93	1	1	2
Q581-13	Q9HAW7-2	UD17_HUMAN	UGT1A7	Isoform 2 of UDP-glucuronosyltransferase 1-7	1.0000	4.76	1	1	2
Q581-14	Q9HAW7	UD17_HUMAN	UGT1A7	UDP-glucuronosyltransferase 1-7	1.0000	3.96	1	1	2
Q581-15	Q9HAW9-2	UD18_HUMAN	UGT1A8	Isoform 2 of UDP-glucuronosyltransferase 1-8	1.0000	4.76	1	1	2
Q581-16	Q9HAW9	UD18_HUMAN	UGT1A8	UDP-glucuronosyltransferase 1-8	1.0000	3.96	1	1	2
Q581-17	O60656-2	UD19_HUMAN	UGT1A9	Isoform 2 of UDP-glucuronosyltransferase 1-9	1.0000	4.76	1	1	2
Q581-18	O60656	UD19_HUMAN	UGT1A9	UDP-glucuronosyltransferase 1-9	1.0000	3.96	1	1	2
						GAGVTUNVLEMTSEDLENALK	2	0.9993	2
Q582-1	Q15019-2	SEPT2_HUMAN	SEPT2	Isoform 2 of Septin-2	1.0000	7.07	2	2	3
Q582-2	Q15019-3	SEPT2_HUMAN	SEPT2	Isoform 3 of Septin-2	1.0000	7.55	2	2	3
Q582-3	B5MCK3	B5MCK3_HUMAN	SEPT2	Septin-2	1.0000	8.72	2	2	3
Q582-4	Q15019	SEPT2_HUMAN	SEPT2	Septin-2	1.0000	7.76	2	2	3
Q582-5	C9IY94	C9IY94_HUMAN	SEPT2	Septin-2 (Fragment)	1.0000	23.14	2	2	3
Q582-6	C9I2U3	C9I2U3_HUMAN	SEPT2	Septin-2 (Fragment)	1.0000	21.37	2	2	3
Q582-7	C9I2Q4	C9I2Q4_HUMAN	SEPT2	Septin-2 (Fragment)	1.0000	15.22	2	2	3
Q582-8	C9I938	C9I938_HUMAN	SEPT2	Septin-2 (Fragment)	1.0000	18.52	2	2	3
Q582-9	C9I825	C9I825_HUMAN	SEPT2	Septin-2 (Fragment)	1.0000	16.18	2	2	3
Q582-10	C9IQJ4	C9IQJ4_HUMAN	SEPT2	Septin-2 (Fragment)	1.0000	19.05	2	2	3
Q582-11	H7C310	H7C310_HUMAN	SEPT2	Septin-2 (Fragment)	1.0000	17.39	2	2	3
						LTVDTPGVGDAINCR	2	0.9991	1
						TIISYDEQFER	2	0.9996	2
Q583-1	B5MD38	B5MD38_HUMAN	HADHB	3-ketoacyl-CoA thiolase	0.9998	4.56	1	1	1
Q583-2	C9JE81	C9JE81_HUMAN	HADHB	Trifunctional enzyme subunit beta, mitochondrial (Fragment)	0.9998	9.14	1	1	1
Q583-3	C9JEY0	C9JEY0_HUMAN	HADHB	Trifunctional enzyme subunit beta, mitochondrial (Fragment)	0.9998	10.74	1	1	1
						EVVDYIIFGTIVQEVK	2	0.9932	1
Q584-1	B5MDF5	B5MDF5_HUMAN	RAN	GTP-binding nuclear protein Ran	0.9860	10.3	2	2	2
Q584-2	P6Z826	RAN_HUMAN	RAN	GTP-binding nuclear protein Ran	0.9860	11.11	2	2	2
Q584-3	J3KQE5	J3KQE5_HUMAN	RAN	GTP-binding nuclear protein Ran (Fragment)	0.9860	10.26	2	2	2
						LVLVGGDGTGK	2	0.8895	1
						VCENIPVLGCGNK	2	0.8728	1
Q585-1	H3BRV0	H3BRV0_HUMAN	EIF3C	Eukaryotic translation initiation factor 3 subunit C	1.0000	5.09	4	4	7
Q585-2	O99613	EIF3C_HUMAN	EIF3C	Eukaryotic translation initiation factor 3 subunit C	1.0000	5.04	4	4	7
Q585-3	B5ME19	EIF3CL_HUMAN	EIF3CL	Eukaryotic translation initiation factor 3 subunit C-like protein	1.0000	5.03	4	4	7
						GCILTIVR	2	0.9993	2
						LGLSVENNER	2	0.9924	2
						TEPTAQQLALQLAEK	2	0.9992	1
						TMVQLGICAFR	2	0.9996	2
Q586-1	B5ME49	B5ME49_HUMAN	MUC16	Mucin-16	0.9815	0.21	2	2	2
Q586-2	Q8W07	MUC16_HUMAN	MUC16	Mucin-16	0.9815	0.14	2	2	2
						SIGSGAESTNLUKISTTR	2	0.8521	1
						VPVGIVTSVTSRR	2	0.84	1
Q587-1	B7WPK3	B7WPK3_HUMAN	FTCD	Formimidoyltransferase-cyclodeaminase	1.0000	19.8	5	6	8
Q587-2	O95954	FTCD_HUMAN	FTCD	Formimidoyltransferase-cyclodeaminase	1.0000	18.11	5	6	8
Q587-3	O95954-3	FTCD_HUMAN	FTCD	Isoform D of Formimidoyltransferase-cyclodeaminase	1.0000	19.8	5	6	8
						GVSVDECVLCAQAFGR	2	0.9985	2
						LAELDVPVLYGEAR	2	0.9967	1
						LGDLSCPSPK	2	0.9797	1
						NQEVDAISGAIQTGPGCVLLDVGDPSTNR	3	0.9664	1
						TVYTFVGPPECVVEGALNAAR	2	0.9984	2
						TVYTFVGPPECVVEGALNAAR	3	0.9894	1
Q588-1	B7Z1C9	B7Z1C9_HUMAN	CCT7	Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a	1.0000	16.87	5	5	8
Q588-2	Q99832-2	TCPH_HUMAN	CCT7	Isoform 2 of T-complex protein 1 subunit eta	1.0000	20.65	5	5	8
Q588-3	Q99832-4	TCPH_HUMAN	CCT7	Isoform 4 of T-complex protein 1 subunit eta	1.0000	15.35	5	5	8
Q588-4	F5GZK5	F5GZK5_HUMAN	CCT7	T-complex protein 1 subunit eta	1.0000	15.8	5	5	8
						CDVFETQIGGER	2	0.9996	2
						GGAEQFMEETER	2	0.9606	1
						IALLNVELEK	2	0.9824	1
						INALTAASEAACLVSVDETINKNPR	3	0.9993	3
						YNNFTGCPK	2	0.9076	1
Q589-1	B7Z1K0	B7Z1K0_HUMAN	BAI3	Brain-specific angiogenesis inhibitor 3	0.9818	6.17	2	2	2
Q589-2	J3KMY8	J3KMY8_HUMAN	BAI3	Brain-specific angiogenesis inhibitor 3	0.9818	4.12	2	2	2
Q589-3	O60242	BAI3_HUMAN	BAI3	Brain-specific angiogenesis inhibitor 3	0.9818	1.97	2	2	2
						DSLQGFVIMVHCILR	2	0.843	1
						SETGSISSMSLER	2	0.8839	1
Q590-1	B7Z1R5	B7Z1R5_HUMAN	ATP6V1A	V-type proton ATPase catalytic subunit A	1.0000	7.36	3	3	4
Q590-2	P38606	VATA_HUMAN	ATP6V1A	V-type proton ATPase catalytic subunit A	1.0000	6.97	3	3	4
Q590-3	C9JA17	C9JA17_HUMAN	ATP6V1A	V-type proton ATPase catalytic subunit A (Fragment)	1.0000	23.37	3	3	4
Q590-4	C9IVW8	C9IVW8_HUMAN	ATP6V1A	V-type proton ATPase catalytic subunit A (Fragment)	1.0000	19.46	3	3	4
						FTMWQVWPVR	2	0.9988	2
						VGHSELVGEIR	3	0.9702	1
						VGSHITGGDIYGVSENSLUK	3	0.9908	1
Q591-1	B7Z2F4	B7Z2F4_HUMAN	CCT4	T-complex protein 1 subunit delta	1.0000	15.42	4	5	9
						ALIAGGGAPEIELAR	2	0.9996	3
						IGLIQFCLSPAK	2	0.9995	2
						LGGTIDDCVELVGLVLTQK	2	0.9992	1
						LGGTIDDCVELVGLVLTQK	3	0.9675	2
						VIDPATATSVDLR	2	0.9966	1
Q592-1	B7Z3Y2	B7Z3Y2_HUMAN	PCYOX1	Prenylcysteine oxidase 1	0.9622	3.04	1	1	1
Q592-2	B7Z9P8	B7Z9P8_HUMAN	PCYOX1	Prenylcysteine oxidase 1	0.9622	3.04	1	1	1
Q592-3	Q9UNG3	PCYOX_HUMAN	PCYOX1	Prenylcysteine oxidase 1	0.9622	2.57	1	1	1
						MYEVVYQIGETR	2	0.9622	1

Q593-1	B72413	B72413_HUMAN	ATP6AP2	Renin receptor	1.0000	34.31	6	7	13
Q593-2	B72913	B72913_HUMAN	ATP6AP2	Renin receptor	1.0000	29.56	6	7	13
Q593-3	Q75787	RENH_HUMAN	ATP6AP2	Renin receptor	1.0000	26.86	6	7	13
Q593-4	H7C3E1	H7C3E1_HUMAN	ATP6AP2	Renin receptor (Fragment)	1.0000	36.29	6	7	13
						ANSVFEDLSVTLR	2	0.9996	3
						DHSPDLYSLLAGLDEIGKR	3	0.8415	1
						FADDMYSLNGGNVAVELTVVK	2	0.9095	3
						FADDMYSLNGGNVAVELTVVK	3	0.9959	1
						ILYDALQK	2	0.9887	1
						NNEVDLLFLSELQVLHDISSLLSR	3	0.9988	3
						SFDTSLIR	2	0.983	1
Q594-1	B724K6	B724K6_HUMAN	DNA5E2	Deoxyribonuclease-2-alpha	1.0000	9.84	2	2	3
Q594-2	O00115	DNS2A_HUMAN	DNA5E2	Deoxyribonuclease-2-alpha	1.0000	8.33	2	2	3
Q594-3	K7EN5	K7EN5_HUMAN	DNA5E2	Deoxyribonuclease-2-alpha (Fragment)	1.0000	13.76	2	2	3
						ALINSPGAVGR	2	0.9992	1
						LTCYGDGSGQPDVWFVYK	2	0.9851	2
Q595-1	B724L4	B724L4_HUMAN	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	0.9834	2.53	1	1	1
Q595-2	P04843	RPN1_HUMAN	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	0.9834	1.81	1	1	1
						SEDLVDYGFPR	2	0.9728	1
Q596-1	B725C0	B725C0_HUMAN	DNAIA1	DnaI homolog subfamily A member 1	0.9794	5.42	1	1	2
Q596-2	P31689	DNAIA1_HUMAN	DNAIA1	DnaI homolog subfamily A member 1	0.9794	3.27	1	1	2
Q596-3	P31689-2	DNAIA1_HUMAN	DNAIA1	isoform 2 of DnaI homolog subfamily A member 1	0.9794	3.93	1	1	2
						TVITSHPGQIVK	2	0.9794	2
Q597-1	B725N8	B725N8_HUMAN	HOXB3	Homeobox protein Hox-B3	0.9199	15.38	1	1	1
Q597-2	B72AD0	B72AD0_HUMAN	HOXB3	Homeobox protein Hox-B3	0.9199	12.85	1	1	1
Q597-3	P14651	HXB3_HUMAN	HOXB3	Homeobox protein Hox-B3	0.9199	10.67	1	1	1
						NNSPGTAGECGGGGGGGGGGGGGGGGGGGGGGDKSPGSAASK	3	0.9199	1
Q598-1	B726Z4	B726Z4_HUMAN	MYL6	Myosin light polypeptide 6	1.0000	18.07	4	4	7
Q598-2	F8W1R7	F8W1R7_HUMAN	MYL6	Myosin light polypeptide 6	1.0000	29.66	4	4	7
Q598-3	J3KND3	J3KND3_HUMAN	MYL6	Myosin light polypeptide 6	1.0000	28.29	4	4	7
Q598-4	P06060	MYL6_HUMAN	MYL6	Myosin light polypeptide 6	1.0000	28.48	4	4	7
						ALGQMPPIAAVLK	2	0.9994	2
						DQGTYYDYVEGLR	2	0.9909	2
						EAFQLFDR	2	0.9981	2
						HVLVTLGK	2	0.9993	1
Q599-1	B727A9	B727A9_HUMAN	PGK1	Phosphoglycerate kinase	1.0000	42.67	14	17	37
Q599-2	P00558	PGK1_HUMAN	PGK1	Phosphoglycerate kinase 1	1.0000	39.81	14	17	37
						ACANPAAGSVILENLR	2	0.9997	4
						ACANPAAGSVILENLR	3	0.9994	3
						AEPKIEAFR	2	0.9662	1
						ALSPERPFLL	2	0.9618	2
						ALSPERPFLLAGGAK	3	0.9995	4
						ALMDEVVK	2	0.9802	1
						GCTTGGGGTATCCAK	2	0.9997	5
						GPVGVFEWFAFAR	2	0.8619	2
						LGDIVYNDAGFAHR	2	0.9923	1
						LGDIVYNDAGFAHR	3	0.9926	1
						QIVWNGPVGVFEWFAFAR	2	0.9997	5
						QIVWNGPVGVFEWFAFAR	3	0.9942	2
						SLGKDVFLK	3	0.9909	2
						VLNNMEIGTSLFDEGAK	2	0.9984	1
						VLPGVDAISNI	2	0.9986	1
						VSHVSTGGGASLELEGK	3	0.9957	1
						WNTEKSHVSTGGGASLELEGK	3	0.8025	1
Q5100-1	B728M7	B728M7_HUMAN	RAB1A	Ras-related protein Rab-1A	1.0000	26.59	3	3	6
Q5100-2	E9PLD0	E9PLD0_HUMAN	RAB1B	Ras-related protein Rab-1B	1.0000	27.22	3	3	6
Q5100-3	Q9H0U4	RAB1B_HUMAN	RAB1B	Ras-related protein Rab-1B	1.0000	22.89	3	3	6
						EFADSLGPIFLETSK	2	0.9674	2
						FAODTYTESYSTIGVDFK	2	0.9994	2
						LLIGDSGVGK	2	0.985	2
Q5101-1	B728Q5	B728Q5_HUMAN	HABP2	Hyaluronan-binding protein 2 50 kDa heavy chain	1.0000	11.07	2	2	4
						FCEIGSDDCYVGDGYSYR	2	0.9996	1
						GQCLITQSPYYR	2	0.9942	3
Q5102-1	B72909	B72909_HUMAN	HYOU1	Hypoxia up-regulated protein 1	0.9304	2.33	1	1	1
Q5102-2	E9PL22	E9PL22_HUMAN	HYOU1	Hypoxia up-regulated protein 1	0.9304	1.39	1	1	1
Q5102-3	Q9Y4L1	HYOU1_HUMAN	HYOU1	Hypoxia up-regulated protein 1	0.9304	1.3	1	1	1
Q5102-4	E9PJ21	E9PJ21_HUMAN	HYOU1	Hypoxia up-regulated protein 1 (Fragment)	0.9304	1.98	1	1	1
						VEFEELCADLFR	2	0.9304	1
Q5103-1	P50991-2	TCFD_HUMAN	CCT4	Isoform 2 of T-complex protein 1 subunit delta	1.0000	14.34	5	7	12
Q5103-2	B729L0	B729L0_HUMAN	CCT4	T-complex protein 1 subunit delta	1.0000	15.11	5	7	12
Q5103-3	P50991	TCFD_HUMAN	CCT4	T-complex protein 1 subunit delta	1.0000	13.54	5	7	12
						ALIAGSGAPEIELAIR	2	0.9996	3
						GIHPTIISFQK	2	0.9916	2
						GIHPTIISFQK	3	0.9302	1
						IGLIQFCLSAK	2	0.9995	2
						LGITDDCELVEGLVLTQK	2	0.9992	1
						LGITDDCELVEGLVLTQK	3	0.9675	2
						VIOPATATSVOLR	2	0.9966	1
Q5104-1	P48643-2	TCPE_HUMAN	CCT5	Isoform 2 of T-complex protein 1 subunit epsilon	1.0000	6.25	2	2	2
Q5104-2	B7ZAR1	B7ZAR1_HUMAN	CCT5	T-complex protein 1 subunit epsilon	1.0000	5.57	2	2	2
Q5104-3	E7EN23	E7EN23_HUMAN	CCT5	T-complex protein 1 subunit epsilon	1.0000	5.76	2	2	2
Q5104-4	E9PCA1	E9PCA1_HUMAN	CCT5	T-complex protein 1 subunit epsilon	1.0000	5.38	2	2	2
Q5104-5	P48643	TCPE_HUMAN	CCT5	T-complex protein 1 subunit epsilon	1.0000	5.18	2	2	2
						DVDFELIKVEGK	2	0.9959	1
						LGFAGLVQEISFGTK	2	0.9955	1
Q5105-1	B7ZC38	B7ZC38_HUMAN	SH3GLB2	Endophilin-B2	0.9978	7.5	2	2	2
Q5105-2	B7ZC39	B7ZC39_HUMAN	SH3GLB2	Endophilin-B2	0.9978	8.02	2	2	2
Q5105-3	F8WFB9	F8WFB9_HUMAN	SH3GLB2	Endophilin-B2	0.9978	23.62	2	2	2
Q5105-4	Q9NR46	SHLB2_HUMAN	SH3GLB2	Endophilin-B2	0.9978	7.59	2	2	2
Q5105-5	Q9NR46-2	SHLB2_HUMAN	SH3GLB2	Isoform 2 of Endophilin-B2	0.9978	7.43	2	2	2
						FGQAEKTELDAAHFNLLAR	3	0.806	1
						LASDAGIFFR	2	0.9884	1
Q5106-1	B7ZKJ8	B7ZKJ8_HUMAN	ITIH4	35 kDa inter-alpha-trypsin inhibitor heavy chain H4	1.0000	19.36	16	17	33
Q5106-2	Q14624	ITIH4_HUMAN	ITIH4	Inter-alpha-trypsin inhibitor heavy chain H4	1.0000	19.46	16	17	33
Q5106-3	Q14624-2	ITIH4_HUMAN	ITIH4	Isoform 2 of inter-alpha-trypsin inhibitor heavy chain H4	1.0000	19.8	16	17	33
Q5106-4	Q14624-3	ITIH4_HUMAN	ITIH4	Isoform 3 of inter-alpha-trypsin inhibitor heavy chain H4	1.0000	20.11	16	17	33
						AGFSWIEVTFK	2	0.9994	4
						ANTVQEATFQMLPK	2	0.9996	4
						DQFNLFVSTEAQWRPSLVPSAEVNVK	3	0.9312	1
						EKAEAAQYSAVAK	2	0.9909	1
						ETLFSVMPGLK	2	0.8496	1
						GLLFDWGR	2	0.9064	1
						ILDDLSR	2	0.9877	1
						ITFELYEELLK	2	0.9995	3
						ITFELYEELLKR	2	0.8653	1
						LGIVYELLK	2	0.9995	3
						QGPVNLISDPEDGVETGQYER	2	0.9996	1
						QGPVNLISDPEDGVETGQYER	3	0.9402	1
						RLDYQEGPPGVSEICWSVEL	2	0.9995	5
						RLGVYELLK	3	0.9989	2
						SDPEQGVETGQYER	2	0.9868	1
						SPEQGVETLDGNLIIR	2	0.9995	2
						VTIGLLFDWGR	2	0.9977	1
Q5107-1	P40925-2	MDHC_HUMAN	MDH1	Isoform 2 of Malate dehydrogenase, cytoplasmic	1.0000	12.65	3	3	4
Q5107-2	P40925-3	MDHC_HUMAN	MDH1	Isoform 3 of Malate dehydrogenase, cytoplasmic	1.0000	8.81	3	3	4
Q5107-3	B8Z251	B8Z251_HUMAN	MDH1	Malate dehydrogenase, cytoplasmic	1.0000	18.34	3	3	4
Q5107-4	B9A041	B9A041_HUMAN	MDH1	Malate dehydrogenase, cytoplasmic	1.0000	14.76	3	3	4
Q5107-5	P40925	MDHC_HUMAN	MDH1	Malate dehydrogenase, cytoplasmic	1.0000	9.28	3	3	4
						FVEGLPINDFSR	2	0.874	2
						GFVITTVQGR	2	0.9973	1
						LGVTANDVK	2	0.965	1
							7	8	21
Q5108-1	B9A064	IGLL5_HUMAN	IGLL5	Immunoglobulin lambda-like polypeptide 5	1.0000	23.36	2	0.9435	1

						ATLVCLISDFYPGAVTVAWK	2	0.9997	4
						ATLVCLISDFYPGAVTVAWK	3	0.9997	5
						CLISDFYPGAVTVAWK	2	0.8947	1
						SYSCQVTHEGSTV	2	0.9899	2
						SYSCQVTHEGSTVE	2	0.9852	2
						SYSCQVTHEGSTVEK	2	0.9997	2
						YAASSYLSLTPGQWK	2	0.9997	4
Q5109-1	Q9P1U1	ARP3B_HUMAN	ACTR3B	Actin-related protein 3B	0.9999	2.63	1	1	2
Q5109-2	Q9P1U1-2	ARP3B_HUMAN	ACTR3B	Isoform 2 of Actin-related protein 3B	0.9999	3.32	1	1	2
Q5109-3	Q9P1U1-3	ARP3B_HUMAN	ACTR3B	Isoform 3 of Actin-related protein 3B	0.9999	3.16	1	1	2
Q5109-4	Q9C0K3	ARP3C_HUMAN	ACTR3C	Actin-related protein 3C	0.9999	5.24	1	1	2
Q5109-5	C9I2N3	C9I2N3_HUMAN	ACTR3C	Actin-related protein 3C (Fragment)	0.9999	4.95	1	1	2
Q5109-6	H7CA11	H7CA11_HUMAN	ACTR3C	Actin-related protein 3C (Fragment)	0.9999	5.29	1	1	2
						DITYFIQQLR	2	0.9994	2
Q5110-1	P43307-2	SSRA_HUMAN	SSR1	Isoform 2 of Translocon-associated protein subunit alpha	0.9856	5.79	1	1	2
Q5110-2	C9I2Q1	C9I2Q1_HUMAN	SSR1	Translocon-associated protein subunit alpha	0.9856	5.03	1	1	2
Q5110-3	C9J3L8	C9J3L8_HUMAN	SSR1	Translocon-associated protein subunit alpha	0.9856	5.66	1	1	2
Q5110-4	C9J5W0	C9J5W0_HUMAN	SSR1	Translocon-associated protein subunit alpha	0.9856	5.64	1	1	2
Q5110-5	E9PAI7	E9PAI7_HUMAN	SSR1	Translocon-associated protein subunit alpha	0.9856	5.15	1	1	2
Q5110-6	F5H5Y2	F5H5Y2_HUMAN	SSR1	Translocon-associated protein subunit alpha	0.9856	5.79	1	1	2
Q5110-7	P43307	SSRA_HUMAN	SSR1	Translocon-associated protein subunit alpha	0.9856	5.24	1	1	2
						GTEDFVESLDASFR	2	0.9856	2
Q5111-1	P35080-2	PROF2_HUMAN	PFN2	Isoform 1b of Profilin-2	1.0000	16.43	2	2	5
Q5111-2	G5E9Q6	G5E9Q6_HUMAN	PFN2	Profilin	1.0000	12.23	2	2	5
Q5111-3	C9J0I7	C9J0I7_HUMAN	PFN2	Profilin-2	1.0000	25.27	2	2	5
						AYELALYLR	2	0.9994	3
						SQGGGPTYNVAAGR	2	0.9996	2
Q5112-1	U3KQA9	U3KQA9_HUMAN		Uncharacterized protein (Fragment)	1.0000	8.47	3	3	6
Q5112-2	U3KQV3	U3KQV3_HUMAN		Uncharacterized protein (Fragment)	1.0000	7.75	3	3	6
Q5112-3	C9JRM1	C9JRM1_HUMAN	RHOA	Transforming protein RhoA	1.0000	23.33	3	3	6
Q5112-4	C9J1T2	C9J1T2_HUMAN	RHOA	Transforming protein RhoA (Fragment)	1.0000	24.42	3	3	6
Q5112-5	E9PLA2	E9PLA2_HUMAN	RHOA	Rho-related GTP-binding protein RhoC	1.0000	31.82	3	3	6
Q5112-6	E9PN11	E9PN11_HUMAN	RHOA	Rho-related GTP-binding protein RhoC (Fragment)	1.0000	16.28	3	3	6
Q5112-7	Q5JRO6	Q5JRO6_HUMAN	RHOA	Rho-related GTP-binding protein RhoC (Fragment)	1.0000	23.08	3	3	6
						KLIVVGDGACGK	2	0.9964	1
						LVIVGDGACGK	2	0.984	2
						TCLLVFSK	2	0.9996	3
Q5113-1	D6RBD7	D6RBD7_HUMAN	EEF1E1	Eukaryotic translation elongation factor 1 epsilon-1	0.9407	6.67	1	1	1
Q5113-2	O43324	MCA3_HUMAN	EEF1E1	Eukaryotic translation elongation factor 1 epsilon-1	0.9407	5.75	1	1	1
Q5113-3	D6RCQ0	D6RCQ0_HUMAN	EEF1E1	Eukaryotic translation elongation factor 1 epsilon-1 (Fragment)	0.9407	10.64	1	1	1
Q5113-4	HOYAL7	HOYAL7_HUMAN	EEF1E1	Eukaryotic translation elongation factor 1 epsilon-1 (Fragment)	0.9407	7.35	1	1	1
Q5113-5	O43324-2	MCA3_HUMAN	EEF1E1	Isoform 2 of Eukaryotic translation elongation factor 1 epsilon-1	0.9407	7.19	1	1	1
Q5113-6	C9J1V9	C9J1V9_HUMAN	EEF1E1-BLOC1S5	HCG2043275	0.9407	6.62	1	1	1
						AVIQQWLEYR	2	0.9407	1
Q5114-1	P840B5	ARF5_HUMAN	ARF5	ADP-ribosylation factor 5	1.0000	17.78	2	2	4
Q5114-2	C9J1Z8	C9J1Z8_HUMAN	ARF5	ADP-ribosylation factor 5 (Fragment)	1.0000	21.23	2	2	4
						ILMVGLDAAGK	2	0.9979	2
						LGEIVTITPTIGFNVETVEYK	2	0.9984	2
Q5115-1	Q02818	NUCB1_HUMAN	NUCB1	Nucleobindin-1	0.9977	5.64	2	2	3
Q5115-2	C9J3C1	C9J3C1_HUMAN	NUCB1	Nucleobindin-1 (Fragment)	0.9977	20.97	2	2	3
Q5115-3	C9JBD3	C9JBD3_HUMAN	NUCB1	Nucleobindin-1 (Fragment)	0.9977	23.64	2	2	3
Q5115-4	C9JK22	C9JK22_HUMAN	NUCB1	Nucleobindin-1 (Fragment)	0.9977	9.74	2	2	3
Q5115-5	H7B21	H7B21_HUMAN	NUCB1	Nucleobindin-1 (Fragment)	0.9977	8.81	2	2	3
						LQAAAEADIK	2	0.956	1
						YLQEVIDVLETDGHR	3	0.9471	2
Q5116-1	C9J3M6	C9J3M6_HUMAN	SLC9C1	Sodium/hydrogen exchanger 10 (Fragment)	0.9458	57.65	1	1	1
						KLFWQILLISPGFLVNYLWHSVSNQLLKPTQWLFSAILVSSD	4	0.9458	1
Q5117-1	C9J4S4	C9J4S4_HUMAN	RAB7A	Ras-related protein Rab-7a	1.0000	14.29	1	1	2
Q5117-2	C9J4V0	C9J4V0_HUMAN	RAB7A	Ras-related protein Rab-7a	1.0000	10.45	1	1	2
						EAINVEQAFQTIAR	2	0.9994	2
Q5118-1	I3LS04	I3LS04_HUMAN	EIF5A	Eukaryotic translation initiation factor 5A-1	1.0000	6.45	1	1	2
Q5118-2	I3L397	I3L397_HUMAN	EIF5A	Eukaryotic translation initiation factor 5A-1 (Fragment)	1.0000	8.22	1	1	2
Q5118-3	C9J7B5	C9J7B5_HUMAN	EIF5A2	Eukaryotic translation initiation factor 5A-2	1.0000	11.01	1	1	2
Q5118-4	F8WCJ1	F8WCJ1_HUMAN	EIF5A2	Eukaryotic translation initiation factor 5A-2	1.0000	11.43	1	1	2
Q5118-5	Q9G2V4	IF5A2_HUMAN	EIF5A2	Eukaryotic translation initiation factor 5A-2	1.0000	7.84	1	1	2
Q5118-6	C9J4W5	C9J4W5_HUMAN	EIF5A2	Eukaryotic translation initiation factor 5A-2 (Fragment)	1.0000	10.43	1	1	2
						VHLVGDIIFTGK	3	0.9992	2
Q5119-1	C9J5S7	C9J5S7_HUMAN	PPIA	Peptidyl-prolyl cis-trans isomerase	1.0000	9.09	1	1	2
Q5119-2	F8WE65	F8WE65_HUMAN	PPIA	Peptidyl-prolyl cis-trans isomerase	1.0000	9.17	1	1	2
						DIADVGEPLGR	2	0.9791	2
Q5120-1	C9J6D1	C9J6D1_HUMAN	NAP1L4	Nucleosome assembly protein 1-like 4 (Fragment)	1.0000	11.8	2	2	3
						FYEEVHDLR	2	0.9994	2
						GIPEFWETIFR	2	0.9989	1
Q5121-1	C9J6K0	C9J6K0_HUMAN	SPP2	Secreted phosphoprotein 24 (Fragment)	1.0000	7.63	1	1	1
						DYYVSTAVCR	2	0.9991	1
Q5122-1	C9JQ45	C9JQ45_HUMAN	PFN2	Profilin	1.0000	12.73	1	1	2
Q5122-2	C9J712	C9J712_HUMAN	PFN2	Profilin-2	1.0000	15.38	1	1	2
Q5122-3	P35080	PROF2_HUMAN	PFN2	Profilin-2	1.0000	10	1	1	2
						SQGGGPTYNVAAGR	2	0.9996	2
Q5123-1	C9J7H8	C9J7H8_HUMAN	LDHB	L-lactate dehydrogenase B chain (Fragment)	1.0000	22.79	2	2	3
Q5123-2	F5H793	F5H793_HUMAN	LDHB	L-lactate dehydrogenase B chain (Fragment)	1.0000	30.39	2	2	3
						LAPVAEEATVPNNK	2	0.9996	2
						SLADELALVDLEK	2	0.9993	1
Q5124-1	C9J753	C9J753_HUMAN	DARS	Aspartate--tRNA ligase, cytoplasmic (Fragment)	1.0000	11.43	2	2	3
Q5124-2	C9JLC1	C9JLC1_HUMAN	DARS	Aspartate--tRNA ligase, cytoplasmic (Fragment)	1.0000	10.99	2	2	3
						IYVISLAEP	2	0.9987	2
						LQSGICHLFR	2	0.964	1
Q5125-1	C9J8S3	C9J8S3_HUMAN	RAB7A	Ras-related protein Rab-7a	1.0000	17.5	2	2	4
Q5125-2	P51149	RAB7A_HUMAN	RAB7A	Ras-related protein Rab-7a	1.0000	13.53	2	2	4
						EAINVEQAFQTIAR	2	0.9994	2
						LVTMQIWDTAGQER	2	0.9989	2
Q5126-1	Q969P0	IGSF8_HUMAN	IGSF8	Immunoglobulin superfamily member 8	1.0000	6.36	3	3	5
Q5126-2	C9J8Z4	C9J8Z4_HUMAN	IGSF8	Immunoglobulin superfamily member 8 (Fragment)	1.0000	12.96	3	3	5
Q5126-3	Q969P0-3	IGSF8_HUMAN	IGSF8	Isoform 3 of Immunoglobulin superfamily member 8	1.0000	7.41	3	3	5
						DTQFSVAVFK	2	0.9993	2
						LQAQDAGIYECHTPSTDTR	3	0.9945	2
						VVAGEVQVQR	2	0.9997	1
Q5127-1	F5H3X9	F5H3X9_HUMAN	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory	1.0000	6.74	4	4	8
Q5127-2	C9J9C1	C9J9C1_HUMAN	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory	1.0000	9.11	4	4	8
						FSVCYPR	2	0.8942	1
						LAGGDWFTSR	2	0.993	4
						TSACGLFSVCYPR	2	0.9992	2
						VKEFCENLSADCR	2	0.9033	1
Q5128-1	C9J9S3	C9J9S3_HUMAN	PPP1CB	Serine/threonine-protein phosphatase (Fragment)	1.0000	21.6	2	2	4
Q5128-2	C9JF48	C9JF48_HUMAN	PPP1CB	Serine/threonine-protein phosphatase (Fragment)	1.0000	19.57	2	2	4
						EIFLSQPILELEAPLK	2	0.9997	3
						IVQMTEAER	2	0.9977	1
Q5129-1	Q16629-2	SRSF7_HUMAN	SRSF7	Isoform 2 of Serine/arginine-rich splicing factor 7	1.0000	34.81	4	5	8
Q5129-2	Q16629-3	SRSF7_HUMAN	SRSF7	Isoform 3 of Serine/arginine-rich splicing factor 7	1.0000	35.61	4	5	8
Q5129-3	Q16629-4	SRSF7_HUMAN	SRSF7	Isoform 4 of Serine/arginine-rich splicing factor 7	1.0000	20.8	4	5	8
Q5129-4	Q16629	SRSF7_HUMAN	SRSF7	Serine/arginine-rich splicing factor 7	1.0000	19.75	4	5	8
Q5129-5	C9JAB2	C9JAB2_HUMAN	SRSF7	Serine/arginine-rich splicing factor 7	1.0000	20	4	5	8
						AFSYGPLR	2	0.9864	1
						NPPGFAFVEFEDPR	2	0.9997	3
						NPPGFAFVEFEDPR	3	0.9993	2
						NPPGFAFVEFEDPRDAEDAVR	3	0.8895	1
						VYVNLGTGAGKGELE	2	0.9991	1
Q5130-1	C9JAK5	C9JAK5_HUMAN	ARF4	ADP-ribosylation factor 4	1.0000	46.41	5	5	7
						DANLLLFANK	2	0.9979	1
						IKQVADLEOK	2	0.9944	1
						MLLYDEL	2	0.9855	1
						NICTFVWDVGGQDR	2	0.9784	2
						TWVVQATCATQGTGLYGLDLWSNELSKR	3	0.999	2

Q5131-1	C9JC84	C9JC84_HUMAN	FGG	Fibrinogen gamma chain	1.0000	51.41	46	51	118
Q5131-2	C9JEU5	C9JEU5_HUMAN	FGG	Fibrinogen gamma chain	1.0000	53.26	46	51	118
						AIQLTYNPDESSKP	2	0.936	1
						AIQLTYNPDESSKPNMIDAATLK	3	0.9968	2
						ALRVELEDWNGR	3	0.9007	1
						ASLTHDSSIR	2	0.9082	1
						ASTPNQVYNGIHWATWK	2	0.9971	4
						CHAGHLNGVYQGGTYSK	3	0.9979	3
						DNCILDER	2	0.9997	5
						DTVQIHDTGK	2	0.999	1
						EASILTHDSSIR	2	0.843	1
						EGFGHLSPTGTTEFWLGNEK	2	0.9997	4
						EGFGHLSPTGTTEFWLGNEK	3	0.9996	4
						FGSYCPTTCGIADFL	2	0.9461	2
						FGSYCPTTCGIADFLSTY	2	0.9962	2
						FGSYCPTTCGIADFLSTYQ	2	0.9834	2
						FGSYCPTTCGIADFLSTYQT	2	0.9978	2
						FGSYCPTTCGIADFLSTYQTK	2	0.9998	7
						FGSYCPTTCGIADFLSTYQTK	3	0.9996	4
						FGSYCPTTCGIADFLSTYQTKV	2	0.9937	2
						GIADFLSTYQTK	2	0.9958	2
						IHLSTQ	2	0.976	1
						IHLSTQSAIPYALR	2	0.9997	4
						IHLSTQSAIPYALR	3	0.9995	2
						IHLSTQSAIPYALRV	2	0.9677	1
						IHLSTQSAIPYALRVELEDWNGR	3	0.997	5
						KEFGHLSPTGTTEFWLGNEK	3	0.9592	2
						KMLEIMKYEASILTHDSSIR	3	0.9918	2
						LDGSVDFK	2	0.9988	4
						LDGSVDFKK	2	0.9991	2
						LGEIYNSNNQK	2	0.9914	1
						LSPTGTTEFWLGNEK	2	0.9199	1
						LTGEGQQHHLGGAK	2	0.9994	2
						MLEEMIMKYEASILTHDSSIR	3	0.9988	3
						OSGLYFIKPLK	2	0.9997	2
						OSGLYFIKPLK	3	0.9664	1
						RLDGSVDFK	2	0.9992	2
						RVELEDWNGR	2	0.9422	1
						RYLQEIYNSNNQK	2	0.8573	1
						SILTHDSSIR	2	0.9949	4
						SPTGTTEFWLGNEK	2	0.9861	3
						STQSAIPYALR	2	0.9526	1
						TGTTEFWLGNEK	2	0.9087	1
						TSTADYAMFK	2	0.9992	1
						VAQLEAQCEPCK	2	0.9997	2
						VAQLEAQCEPCKD	2	0.9969	2
						VAQLEAQCEPCKD	2	0.9829	2
						VAQLEAQCEPCKD	2	0.9777	2
						VAQLEAQCEPCKDTVQIHDTGK	3	0.9987	3
						VELEDWNGR	2	0.9996	2
						YEASILTHDSSIR	2	0.9997	4
						YEASILTHDSSIR	3	0.9956	1
						YLQEIYNSNNQK	2	0.9997	3
Q5132-1	C9JCK5	C9JCK5_HUMAN	PSMA2	Proteasome subunit alpha type-2	0.9729	11.59	1	1	3
Q5132-2	P25787	PSA2_HUMAN	PSMA2	Proteasome subunit alpha type-2	0.9729	8.12	1	1	3
						YNEDELEDAIHTAILTK	3	0.9729	3
Q5133-1	P50053-2	KHK_HUMAN	KHK	Isoform C of Kethexokinase	0.9715	4.03	1	1	1
Q5133-2	C9JDL1	C9JDL1_HUMAN	KHK	Kethexokinase (Fragment)	0.9715	4.3	1	1	1
						GVDSVQVWQSK	2	0.9715	1
Q5134-1	C9JEV6	C9JEV6_HUMAN	NAGK	N-acetyl-D-glucosamine kinase	1.0000	9.22	2	2	3
						EGFLALTQGR	2	0.8813	1
						SLGLSLSGDQEDAGR	2	0.9996	2
Q5135-1	C9JF17	C9JF17_HUMAN	APOD	Apolipoprotein D (Fragment)	1.0000	36.28	14	19	54
						CPNPPVQENFDVVK	2	0.9997	5
						CPNPPVQENFDVVK	3	0.9993	2
						CPNPPVQENFDVVKYLGR	2	0.9995	5
						CPNPPVQENFDVVKYLGR	3	0.9994	3
Q5136-1	J3KR4	J3KR4_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	7.91	2	2	2
Q5136-2	J3KR4	J3KR4_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	7.91	2	2	2
Q5136-3	J3K5A5	J3K5A5_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	9.52	2	2	2
Q5136-4	J3K7B0	J3K7B0_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	14.39	2	2	2
Q5136-5	J3QL53	J3QL53_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	11.9	2	2	2
Q5136-6	J3QL58	J3QL58_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	12.05	2	2	2
Q5136-7	J3QL70	J3QL70_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	11.9	2	2	2
Q5136-8	J3QS84	J3QS84_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	19.8	2	2	2
Q5136-9	J3QS88	J3QS88_HUMAN	GP51	COP9 signalosome complex subunit 1 (Fragment)	0.9994	14.93	2	2	2
Q5136-10	Q13098-7	CSN1_HUMAN	GP51	Isoform 2 of COP9 signalosome complex subunit 1	0.9994	3.8	2	2	2
Q5136-11	Q13098-8	CSN1_HUMAN	GP51	Isoform 3 of COP9 signalosome complex subunit 1	0.9994	4.11	2	2	2
Q5136-12	Q13098-9	CSN1_HUMAN	GP51	Isoform 4 of COP9 signalosome complex subunit 1	0.9994	4.11	2	2	2
Q5136-13	Q13098-10	CSN1_HUMAN	GP51	Isoform 5 of COP9 signalosome complex subunit 1	0.9994	4.11	2	2	2
						LOFIADHCPTLR	3	0.9428	1
						MAISVQR	2	0.9893	1
Q5137-1	C9J51	C9J51_HUMAN	GNB2	Guanine nucleotide-binding protein G(i)/G(s)/G(t) subunit beta	1.0000	5.17	1	1	1
Q5137-2	C9JXAS	C9JXAS_HUMAN	GNB2	Guanine nucleotide-binding protein G(i)/G(s)/G(t) subunit beta	1.0000	4.78	1	1	1
						TFVSGACDASIK	2	0.9995	1
Q5138-1	C9JLK0	C9JLK0_HUMAN	ATIC	Phosphoribosylaminoimidazolecarboxamide formyltransferase	1.0000	10.59	2	2	5
						LDNFLIR	2	0.9996	2
						VVACNLVPVK	2	0.9995	3
Q5139-1	Q92841-1	DDX17_HUMAN	DDX17	Isoform 2 of Probable ATP-dependent RNA helicase DDX17	0.9998	1.38	1	1	2
Q5139-2	Q92841-2	DDX17_HUMAN	DDX17	Isoform 3 of Probable ATP-dependent RNA helicase DDX17	0.9998	1.38	1	1	2
Q5139-3	Q92841-3	DDX17_HUMAN	DDX17	Isoform 4 of Probable ATP-dependent RNA helicase DDX17	0.9998	1.38	1	1	2
Q5139-4	Q9JMU5	Q9JMU5_HUMAN	DDX17	Probable ATP-dependent RNA helicase DDX17	0.9998	1.38	1	1	2
Q5139-5	H3BL28	H3BL28_HUMAN	DDX17	Probable ATP-dependent RNA helicase DDX17	0.9998	1.23	1	1	2
Q5139-6	Q92841	DDX17_HUMAN	DDX17	Probable ATP-dependent RNA helicase DDX17	0.9998	1.23	1	1	2
						LDLFESGK	2	0.9406	2
Q5140-1	C9JX21	C9JX21_HUMAN	RHOA	Transforming protein RhoA	1.0000	19.25	4	4	8
Q5140-2	C9JNR4	C9JNR4_HUMAN	RHOA	Transforming protein RhoA (Fragment)	1.0000	27.91	4	4	8
Q5140-3	Q5JRO5	Q5JRO5_HUMAN	RHOC	Rho-related GTP-binding protein Rhoc	1.0000	18.09	4	4	8
Q5140-4	Q5JRO7	Q5JRO7_HUMAN	RHOC	Rho-related GTP-binding protein Rhoc (Fragment)	1.0000	28.35	4	4	8
						HFCPNVPILVGNNK	3	0.9995	2
						KLVIIVGDGACGK	2	0.9964	1
						LVIVGDGACGK	2	0.984	2
						TCLIVF5K	2	0.9996	3
Q5141-1	C9JPM4	C9JPM4_HUMAN	ARF4	ADP-ribosylation factor 4 (Fragment)	1.0000	13.07	3	3	5
						ILMVGDLDAAGK	2	0.9979	2
						IQEVADELQK	2	0.9944	1
						LGEIVTPIPTIGFNVETVEYK	2	0.9984	2
Q5142-1	C9IQM9	C9IQM9_HUMAN	DARS	Aspartate--tRNA ligase, cytoplasmic (Fragment)	1.0000	7.41	1	1	2

						IYVSLAEPR	2	0.9987	2
Q5143-1	Q9NTK5-3	OLA1_HUMAN	OLA1	Isoform 3 of Olg-like ATPase 1	1.0000	5.4	1	2	4
Q5143-2	C9JTK6	C9JTK6_HUMAN	OLA1	Olg-like ATPase 1 (Fragment)	1.0000	12.93	1	2	4
						IPAFNLVVVDIAGLVK	2	0.9997	3
						IPAFNLVVVDIAGLVK	3	0.9488	1
Q5144-1	C9JVN1	C9JVN1_HUMAN	MF12	Melanotransferrin (Fragment)	1.0000	8.84	1	1	3
						TVGWNVPVGYLVESGR	2	0.9994	3
Q5145-1	Q15233-2	NONO_HUMAN	NONO	Isoform 2 of Non-POU domain-containing octamer-binding protein	0.9511	3.66	1	1	2
Q5145-2	Q15233	NONO_HUMAN	NONO	Non-POU domain-containing octamer-binding protein	0.9511	2.97	1	1	2
Q5145-3	C9JY58	C9JY58_HUMAN	NONO	Non-POU domain-containing octamer-binding protein (Fragment)	0.9511	5.67	1	1	2
Q5145-4	H7C367	H7C367_HUMAN	NONO	Non-POU domain-containing octamer-binding protein (Fragment)	0.9511	5.98	1	1	2
						FAQQGSFEYEVAMR	2	0.9511	2
Q5146-1	P13010	XRCC5_HUMAN	XRCC5	X-ray repair cross-complementing protein 5	0.9472	1.5	1	1	1
Q5146-2	C9JZ81	C9JZ81_HUMAN	XRCC5	X-ray repair cross-complementing protein 5 (Fragment)	0.9472	8.4	1	1	1
						HIEIFTDLSSR	2	0.9472	1
Q5147-1	P62256-2	UBE2H_HUMAN	UBE2H	Isoform 2 of Ubiquitin-conjugating enzyme E2 H	1.0000	19.74	2	3	4
Q5147-2	P62256	UBE2H_HUMAN	UBE2H	Ubiquitin-conjugating enzyme E2 H	1.0000	16.39	2	3	4
Q5147-3	C9JZG9	C9JZG9_HUMAN	UBE2H	Ubiquitin-conjugating enzyme E2 H (Fragment)	1.0000	29.13	2	3	4
Q5147-4	C9JZY6	C9JZY6_HUMAN	UBE2H	Ubiquitin-conjugating enzyme E2 H (Fragment)	1.0000	24.39	2	3	4
Q5147-5	H7C4M9	H7C4M9_HUMAN	UBE2H	Ubiquitin-conjugating enzyme E2 H (Fragment)	1.0000	48.39	2	3	4
						FYGPQPTVEGGVWK	2	0.9718	1
						HEVTILGGLNEFVK	2	0.9915	1
						HEVTILGGLNEFVK	3	0.9955	2
Q5148-1	C9JZP6	C9JZP6_HUMAN	DHRS2	Dehydrogenase/reductase SDR family member 2, mitochondrial	1.0000	40.44	8	8	11
Q5148-2	Q13268-2	DHRS2_HUMAN	DHRS2	Isoform 2 of Dehydrogenase/reductase SDR family member 2	1.0000	30.33	8	8	11
						AGIVCHVGK	2	0.886	1
						LQEGGLSVAGIVCHVGK	3	0.9921	1
						LSVAGIVCHVGK	2	0.9442	1
						SAGVNPVLVSTLGTSEQIWDK	2	0.9922	1
						SPALLSQLLPYMENRR	3	0.9954	2
						TLALEAPK	2	0.9656	1
						VAVVGTSTSGISFAIR	2	0.9996	3
						VNCVVPGIK	2	0.9975	1
Q5149-1	C9JZR2	C9JZR2_HUMAN	CTNND1	Catenin delta-1	0.9943	1.92	2	2	2
Q5149-2	O60716	CTND1_HUMAN	CTNND1	Catenin delta-1	0.9943	1.86	2	2	2
Q5149-3	O60716-8	CTND1_HUMAN	CTNND1	Isoform 1 of Catenin delta-1	0.9943	1.97	2	2	2
Q5149-4	O60716-5	CTND1_HUMAN	CTNND1	Isoform 1A of Catenin delta-1	0.9943	1.93	2	2	2
Q5149-5	O60716-2	CTND1_HUMAN	CTNND1	Isoform 1AB of Catenin delta-1	0.9943	1.87	2	2	2
Q5149-6	O60716-3	CTND1_HUMAN	CTNND1	Isoform 1AC of Catenin delta-1	0.9943	1.92	2	2	2
Q5149-7	O60716-6	CTND1_HUMAN	CTNND1	Isoform 1B of Catenin delta-1	0.9943	1.91	2	2	2
Q5149-8	O60716-4	CTND1_HUMAN	CTNND1	Isoform 1BC of Catenin delta-1	0.9943	1.9	2	2	2
Q5149-9	O60716-7	CTND1_HUMAN	CTNND1	Isoform 1C of Catenin delta-1	0.9943	1.96	2	2	2
Q5149-10	O60716-16	CTND1_HUMAN	CTNND1	Isoform 2 of Catenin delta-1	0.9943	2.1	2	2	2
Q5149-11	O60716-13	CTND1_HUMAN	CTNND1	Isoform 2A of Catenin delta-1	0.9943	2.05	2	2	2
Q5149-12	O60716-10	CTND1_HUMAN	CTNND1	Isoform 2AB of Catenin delta-1	0.9943	1.98	2	2	2
Q5149-13	O60716-9	CTND1_HUMAN	CTNND1	Isoform 2ABC of Catenin delta-1	0.9943	1.97	2	2	2
Q5149-14	O60716-11	CTND1_HUMAN	CTNND1	Isoform 2AC of Catenin delta-1	0.9943	2.03	2	2	2
Q5149-15	O60716-14	CTND1_HUMAN	CTNND1	Isoform 2B of Catenin delta-1	0.9943	2.03	2	2	2
Q5149-16	O60716-12	CTND1_HUMAN	CTNND1	Isoform 2BC of Catenin delta-1	0.9943	2.02	2	2	2
Q5149-17	O60716-15	CTND1_HUMAN	CTNND1	Isoform 2C of Catenin delta-1	0.9943	2.08	2	2	2
Q5149-18	O60716-24	CTND1_HUMAN	CTNND1	Isoform 3 of Catenin delta-1	0.9943	2.22	2	2	2
Q5149-19	O60716-21	CTND1_HUMAN	CTNND1	Isoform 3A of Catenin delta-1	0.9943	2.16	2	2	2
Q5149-20	O60716-18	CTND1_HUMAN	CTNND1	Isoform 3AB of Catenin delta-1	0.9943	2.09	2	2	2
Q5149-21	O60716-17	CTND1_HUMAN	CTNND1	Isoform 3ABC of Catenin delta-1	0.9943	2.08	2	2	2
Q5149-22	O60716-19	CTND1_HUMAN	CTNND1	Isoform 3AC of Catenin delta-1	0.9943	2.15	2	2	2
Q5149-23	O60716-22	CTND1_HUMAN	CTNND1	Isoform 3B of Catenin delta-1	0.9943	2.14	2	2	2
Q5149-24	O60716-20	CTND1_HUMAN	CTNND1	Isoform 3BC of Catenin delta-1	0.9943	2.13	2	2	2
Q5149-25	O60716-23	CTND1_HUMAN	CTNND1	Isoform 3C of Catenin delta-1	0.9943	2.2	2	2	2
Q5149-26	O60716-32	CTND1_HUMAN	CTNND1	Isoform 4 of Catenin delta-1	0.9943	3.06	2	2	2
Q5149-27	O60716-29	CTND1_HUMAN	CTNND1	Isoform 4A of Catenin delta-1	0.9943	2.95	2	2	2
Q5149-28	O60716-26	CTND1_HUMAN	CTNND1	Isoform 4AB of Catenin delta-1	0.9943	2.82	2	2	2
Q5149-29	O60716-25	CTND1_HUMAN	CTNND1	Isoform 4ABC of Catenin delta-1	0.9943	2.79	2	2	2
Q5149-30	O60716-27	CTND1_HUMAN	CTNND1	Isoform 4AC of Catenin delta-1	0.9943	2.92	2	2	2
Q5149-31	O60716-30	CTND1_HUMAN	CTNND1	Isoform 4B of Catenin delta-1	0.9943	2.91	2	2	2
Q5149-32	O60716-28	CTND1_HUMAN	CTNND1	Isoform 4BC of Catenin delta-1	0.9943	2.88	2	2	2
Q5149-33	O60716-31	CTND1_HUMAN	CTNND1	Isoform 4C of Catenin delta-1	0.9943	3.03	2	2	2
						LVENCVCLLR	2	0.8892	1
						NLSQVHR	2	0.9485	1
Q5150-1	F8W727	F8W727_HUMAN	RPL32	60S ribosomal protein L32	0.9753	8.5	1	1	2
Q5150-2	P62910	RPL32_HUMAN	RPL32	60S ribosomal protein L32	0.9753	9.63	1	1	2
Q5150-3	D3YT81	D3YT81_HUMAN	RPL32	60S ribosomal protein L32 (Fragment)	0.9753	9.77	1	1	2
						SYCAEIAHNVSSK	2	0.9753	2
Q5151-1	D6R934	D6R934_HUMAN	C1QB	Complement C1q subcomponent subunit B	1.0000	25.9	6	7	8
Q5151-2	P02746	C1QB_HUMAN	C1QB	Complement C1q subcomponent subunit B	1.0000	25.69	6	7	8
						DYAYNTFQVTTGGMVLK	2	0.9529	1
						IAFSATR	2	0.9987	1
						LEOGENVFLQATOK	2	0.9997	1
						TINVPILRR	2	0.9825	1
						VPGLYYFTYHASSR	2	0.9964	1
						VVTFCDYAYNTFQVTTGGMVLK	2	0.9847	2
						VVTFCDYAYNTFQVTTGGMVLK	3	0.898	1
Q5152-1	D6R938	D6R938_HUMAN	CAMK2D	Calcium/calmodulin-dependent protein kinase (CaM kinase)	1.0000	7.63	2	2	2
Q5152-2	E9P8G7	E9P8G7_HUMAN	CAMK2D	Calcium/calmodulin-dependent protein kinase type II subunit	1.0000	7.42	2	2	2
Q5152-3	E9P8F2	E9P8F2_HUMAN	CAMK2D	Calcium/calmodulin-dependent protein kinase type II subunit	1.0000	7.13	2	2	2
Q5152-4	Q13557	KCC2D_HUMAN	CAMK2D	Calcium/calmodulin-dependent protein kinase type II subunit	1.0000	7.62	2	2	2
Q5152-5	Q13557-10	KCC2D_HUMAN	CAMK2D	Isoform Delta 10 of Calcium/calmodulin-dependent protein kinase	1.0000	7.72	2	2	2
Q5152-6	Q13557-11	KCC2D_HUMAN	CAMK2D	Isoform Delta 11 of Calcium/calmodulin-dependent protein kinase	1.0000	7.25	2	2	2
Q5152-7	Q13557-12	KCC2D_HUMAN	CAMK2D	Isoform Delta 12 of Calcium/calmodulin-dependent protein kinase	1.0000	7.95	2	2	2
Q5152-8	Q13557-3	KCC2D_HUMAN	CAMK2D	Isoform Delta 3 of Calcium/calmodulin-dependent protein kinase	1.0000	7.45	2	2	2
Q5152-9	Q13557-4	KCC2D_HUMAN	CAMK2D	Isoform Delta 4 of Calcium/calmodulin-dependent protein kinase	1.0000	7.32	2	2	2
Q5152-10	Q13557-8	KCC2D_HUMAN	CAMK2D	Isoform Delta 6 of Calcium/calmodulin-dependent protein kinase	1.0000	7.95	2	2	2
Q5152-11	Q13557-9	KCC2D_HUMAN	CAMK2D	Isoform Delta 7 of Calcium/calmodulin-dependent protein kinase	1.0000	7.77	2	2	2
Q5152-12	Q13557-5	KCC2D_HUMAN	CAMK2D	Isoform Delta 8 of Calcium/calmodulin-dependent protein kinase	1.0000	7.63	2	2	2
Q5152-13	Q13557-6	KCC2D_HUMAN	CAMK2D	Isoform Delta 9 of Calcium/calmodulin-dependent protein kinase	1.0000	7.41	2	2	2
						FTDEVOLFEELOGK	2	0.9997	1
						ICDPGLTAPEFALGNLVGMDFHR	3	0.9941	1
Q5153-1	P26583	HMG82_HUMAN	HMG82	High mobility group protein B2	0.9738	6.22	1	1	1
Q5153-2	D6R9A6	D6R9A6_HUMAN	HMG82	High mobility group protein B2 (Fragment)	0.9738	9.7	1	1	1
						SEHPGLSIGDTAK	2	0.9529	1
Q5154-1	P10451-3	OSTP_HUMAN	SPP1	Isoform C of Osteopontin	1.0000	9.06	3	3	28
Q5154-2	D6R9C5	D6R9C5_HUMAN	SPP1	Osteopontin (Fragment)	1.0000	10.79	3	3	28
						AIPVAQQLNAPSDWDSR	2	0.9997	22
						GDSVVYGLR	2	0.9997	3
						LNAPSDWDSR	2	0.9849	3
Q5155-1	D6RBF6	D6RBF6_HUMAN	BDH2	3-hydroxybutyrate dehydrogenase type 2	1.0000	32.81	1	1	3
Q5155-2	D6RFG2	D6RFG2_HUMAN	BDH2	3-hydroxybutyrate dehydrogenase type 2	1.0000	23.33	1	1	3
Q5155-3	D6RRJ8	D6RRJ8_HUMAN	BDH2	3-hydroxybutyrate dehydrogenase type 2 (Fragment)	1.0000	18.1	1	1	3
Q5155-4	D6RIR6	D6RIR6_HUMAN	BDH2	3-hydroxybutyrate dehydrogenase type 2 (Fragment)	1.0000	16.15	1	1	3
Q5155-5	Q9BU11-2	BDH2_HUMAN	BDH2	Isoform 2 of 3-hydroxybutyrate dehydrogenase type 2	1.0000	12.14	1	1	3
						VIILTAAAGIGQAAALAFAR	3	0.9996	3
Q5156-1	D6RA82	D6RA82_HUMAN	ANXA3	Annexin	0.9999	4.58	1	1	1
Q5156-2	P12429	ANXA3_HUMAN	ANXA3	Annexin A3	0.9999	4.02	1	1	1
						SDTSGDYEIFLLK	2	0.9876	1
Q5157-1	D6RAC2	D6RAC2_HUMAN	GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1	1.0000	7.81	2	2	3
Q5157-2	D6RF23	D6RF23_HUMAN	GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1	1.0000	20.79	2	2	3
Q5157-3	HOY8R5	HOY8R5_HUMAN	GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)	1.0000	15.22	2	2	3
						VWQVTIGTR	2	0.9992	2
						YWLCATGPSIK	2	0.9997	1
Q5158-1	D6RAT0	D6RAT0_HUMAN	RPS3A	40S ribosomal protein S3a	0.9467	7.49	1	1	1
Q5158-2	D6RI02	D6RI02_HUMAN	RPS3A	40S ribosomal protein S3a	0.9467	17.89	1	1	1
Q5158-3	E9PFI5	E9PFI5_HUMAN	RPS3A	40S ribosomal protein S3a	0.9467	8.29	1	1	1
Q5158-4	FSH4F9	FSH4F9_HUMAN	RPS3A	40S ribosomal protein S3a	0.9467	9.71	1	1	1
Q5158-5	P61247	RS3A_HUMAN	RPS3A	40S ribosomal protein S3a	0.9467	6.44	1	1	1

Q5158-6	D6RAS7	D6RAS7_HUMAN	RP53A	40S ribosomal protein S3a (Fragment)	0.9467	13.6	1	1	1
Q5158-7	D6RB09	D6RB09_HUMAN	RP53A	40S ribosomal protein S3a (Fragment)	0.9467	8.81	1	1	1
Q5158-8	D6RED7	D6RED7_HUMAN	RP53A	40S ribosomal protein S3a (Fragment)	0.9467	16.83	1	1	1
Q5158-9	D6RG13	D6RG13_HUMAN	RP53A	40S ribosomal protein S3a (Fragment)	0.9467	7.62	1	1	1
Q5158-10	D6RGE0	D6RGE0_HUMAN	RP53A	40S ribosomal protein S3a (Fragment)	0.9467	26.15	1	1	1
Q5158-11	HOY8L7	HOY8L7_HUMAN	RP53A	40S ribosomal protein S3a (Fragment)	0.9467	8.95	1	1	1
Q5159-1	D6RAX7	D6RAX7_HUMAN	COP54	COP9 signalosome complex subunit 4	1.0000	VFEVSLADLQNDVAFR	2	0.9467	1
Q5159-2	D6RFN0	D6RFN0_HUMAN	COP54	COP9 signalosome complex subunit 4	1.0000	10	3	4	6
Q5159-3	Q9BT78	CSN4_HUMAN	COP54	COP9 signalosome complex subunit 4	1.0000	9.59	3	4	6
						10.34	3	4	6
						COQLAAYGILEK	2	0.857	1
						IASQMITEGR	2	0.9894	2
						LYNNITFEELGALLEIPAAK	2	0.9994	1
						LYNNITFEELGALLEIPAAK	3	0.999	2
Q5160-1	D6RBV2	D6RBV2_HUMAN	LMAN2	Vesicular integral-membrane protein VIP36	1.0000	48	21	26	75
Q5160-2	Q12907	LMAN2_HUMAN	LMAN2	Vesicular integral-membrane protein VIP36	1.0000	43.82	21	26	75
						DGIALWYTR	2	0.8412	2
						DHDTFLAVR	2	0.9995	2
						DHDTGNSHLKR	2	0.9681	1
						DNFHGLAIFLDTPYNDETTER	2	0.9997	2
						DLRVPGPVFGSK	2	0.999	2
						DLRVPGPVFGSK	3	0.9986	2
						DLRVPGPVFGSKDNFHGLAIFLDTPYNDETTER	4	0.9637	1
						DTYPNDETTER	2	0.9856	4
						LAGCTADFR	2	0.8968	1
						LDTPNDETTER	2	0.967	2
						LFQLMVEHTPDDESIDWTK	2	0.9997	1
						LFQLMVEHTPDDESIDWTK	3	0.9992	3
						LPTGYFGASAGTGDLSNDHDIISMK	3	0.9997	12
						LTVMTDLEKNEWK	2	0.9995	4
						LTVMTDLEKNEWK	3	0.921	1
						LVPVPGVFGSK	2	0.997	1
						LVPVPGVFGSKDNFHGLAIFLDTPYNDETTER	3	0.9969	4
						NCIDITGVR	2	0.9993	2
						NCIDITGVRPLPTG	2	0.9302	1
						NCIDITGVRPLPTGY	2	0.8746	1
						NLHGDGIALWYTR	2	0.9996	4
						NLHGDGIALWYTR	3	0.9994	5
						NRDHDFTFLAVR	2	0.9989	3
						NRDHDFTFLAVR	3	0.9994	4
						VFPYISV	2	0.8189	1
						WTLAGCTADFR	2	0.9998	9
Q5161-1	D6RD47	D6RD47_HUMAN	RP523	40S ribosomal protein S23	0.9993	8.96	2	2	2
Q5161-2	P62266	RS23_HUMAN	RP523	40S ribosomal protein S23	0.9993	6.39	2	2	2
						GHAHGQIGVGR	2	0.9328	1
						KGHAVGQIGVGR	2	0.9894	1
Q5162-1	D6RD63	D6RD63_HUMAN	COP54	COP9 signalosome complex subunit 4 (Fragment)	1.0000	15.27	3	3	4
						COQLAAYGILEK	2	0.857	1
						IASQMITEGR	2	0.9894	2
						LYNNITFEELGALLEIPAAK	2	0.9994	1
Q5163-1	D6RD66	D6RD66_HUMAN	WDR1	WD repeat-containing protein 1 (Fragment)	1.0000	19.59	4	4	8
						DIAWTEDSKR	2	0.9981	2
						DIYTEHAHQVVVAK	2	0.9728	1
						IAVVGEGR	2	0.9996	2
						YAPSGFYIASGVSGK	2	0.9997	3
Q5164-1	P20290-2	BTF3_HUMAN	BTF3	Isoform 2 of Transcription factor BTF3	0.9867	11.73	1	1	1
Q5164-2	P20290	BTF3_HUMAN	BTF3	Transcription factor BTF3	0.9867	9.22	1	1	1
Q5164-3	D6RDG3	D6RDG3_HUMAN	BTF3	Transcription factor BTF3 (Fragment)	0.9867	17.27	1	1	1
Q5164-4	HOY9Y1	HOY9Y1_HUMAN	BTF3	Transcription factor BTF3 (Fragment)	0.9867	22.09	1	1	1
						VQASLAANTFITTIGHAETK	2	0.9867	1
Q5165-1	D6RE86	D6RE86_HUMAN	CP	Ceruloplasmin (Fragment)	1.0000	6.74	1	1	2
						ALVLYQYTDETR	2	0.9993	2
Q5166-1	P31040-2	SDHA_HUMAN	SDHA	Isoform 2 of Succinate dehydrogenase (ubiquinone) flavoprotein subunit	0.9850	2.27	1	1	2
Q5166-2	P31040-3	SDHA_HUMAN	SDHA	Isoform 3 of Succinate dehydrogenase (ubiquinone) flavoprotein subunit	0.9850	2.7	1	1	2
Q5166-3	D6RFM5	D6RFM5_HUMAN	SDHA	Succinate dehydrogenase (ubiquinone) flavoprotein subunit	0.9850	2.4	1	1	2
Q5166-4	P31040	SDHA_HUMAN	SDHA	Succinate dehydrogenase (ubiquinone) flavoprotein subunit	0.9850	2.11	1	1	2
Q5166-5	HOY8X1	HOY8X1_HUMAN	SDHA	Succinate dehydrogenase (ubiquinone) flavoprotein subunit	0.9850	11.11	1	1	2
						LGANSLLDLVVFGR	2	0.985	2
Q5167-1	D6RG11	D6RG11_HUMAN	C1Q8	Complement C1q subcomponent subunit 8 (Fragment)	1.0000	9.8	2	2	2
						IAFSATR	2	0.9987	1
						TINVPRLRR	2	0.9825	1
Q5168-1	D6RH8	D6RH8_HUMAN	HPGD	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	1.0000	59.46	2	2	3
Q5168-2	E9PD69	E9PD69_HUMAN	HPGD	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	1.0000	25.29	2	2	3
						AFEAALLK	2	0.9996	2
						VALVTGAAQIGIR	2	0.9997	1
Q5171-1	P00915	CAH1_HUMAN	CA1	Carbonic anhydrase 1	1.0000	13.41	3	3	5
Q5171-2	ESRFE7	ESRFE7_HUMAN	CA1	Carbonic anhydrase 1 (Fragment)	1.0000	18.04	3	3	5
Q5171-3	ESRHP7	ESRHP7_HUMAN	CA1	Carbonic anhydrase 1 (Fragment)	1.0000	13.94	3	3	5
Q5171-4	ESRIJ8	ESRIJ8_HUMAN	CA1	Carbonic anhydrase 1 (Fragment)	1.0000	25.55	3	3	5
						ADGLAVIGVLMK	2	0.993	2
						ESISVSSEQLAQFR	2	0.9989	2
						VLDAIQAIR	2	0.8972	1
Q5172-1	HOYNP0	HOYNP0_HUMAN	CYIFP1	Cytoplasmic FMRI-interacting protein 1	1.0000	11.69	1	1	1
Q5172-2	Q7L576	CYFP1_HUMAN	CYIFP1	Cytoplasmic FMRI-interacting protein 1	1.0000	0.72	1	1	1
Q5172-3	HOYL39	HOYL39_HUMAN	CYIFP1	Cytoplasmic FMRI-interacting protein 1 (Fragment)	1.0000	5.59	1	1	1
Q5172-4	HOYL5	HOYL5_HUMAN	CYIFP1	Cytoplasmic FMRI-interacting protein 1 (Fragment)	1.0000	5.96	1	1	1
Q5172-5	ESRFQ0	ESRFQ0_HUMAN	CYIFP2	Cytoplasmic FMRI-interacting protein 2	1.0000	9.47	1	1	1
Q5172-6	ESRUW3	ESRUW3_HUMAN	CYIFP2	Cytoplasmic FMRI-interacting protein 2	1.0000	12.68	1	1	1
Q5172-7	E7EVF4	E7EVF4_HUMAN	CYIFP2	Cytoplasmic FMRI-interacting protein 2	1.0000	0.72	1	1	1
Q5172-8	E7EVJ5	E7EVJ5_HUMAN	CYIFP2	Cytoplasmic FMRI-interacting protein 2	1.0000	0.73	1	1	1
Q5172-9	E7EWA4	E7EWA4_HUMAN	CYIFP2	Cytoplasmic FMRI-interacting protein 2	1.0000	0.7	1	1	1
Q5172-10	Q9GF07	CYFP2_HUMAN	CYIFP2	Cytoplasmic FMRI-interacting protein 2	1.0000	0.7	1	1	1
Q5172-11	Q9GF07-2	CYFP2_HUMAN	CYIFP2	Isoform 2 of Cytoplasmic FMRI-interacting protein 2	1.0000	0.72	1	1	1
Q5172-12	E7EW33	E7EW33_HUMAN	CYIFP2	Uncharacterized protein	1.0000	0.85	1	1	1
						NAPVTGIAR	2	0.9885	1
Q5173-1	QBWX9-2	SREK1_HUMAN	SREK1	Isoform 2 of Splicing regulatory glutamine/lysine-rich protein	0.9856	2.08	1	1	1
Q5173-2	ESRFV3	ESRFV3_HUMAN	SREK1	Splicing regulatory glutamine/lysine-rich protein 1	0.9856	9.85	1	1	1
						TLFSFGEIEELR	2	0.9856	1
Q5174-1	Q9Y646	CBPQ_HUMAN	CPQ	Carboxypeptidase Q	1.0000	4.45	2	2	2
Q5174-2	ESRH35	ESRH35_HUMAN	CPQ	Carboxypeptidase Q (Fragment)	1.0000	16.15	2	2	2
Q5174-3	ESRIJ8	ESRIJ8_HUMAN	CPQ	Carboxypeptidase Q (Fragment)	1.0000	11.29	2	2	2
Q5174-4	ESRIJ8	ESRIJ8_HUMAN	CPQ	Carboxypeptidase Q (Fragment)	1.0000	15.33	2	2	2
Q5174-5	ESRIJ7	ESRIJ7_HUMAN	CPQ	Carboxypeptidase Q (Fragment)	1.0000	16.03	2	2	2
						AINLAVYVK	2	0.9735	1
						LALLVDVTGPR	2	0.9994	1
Q5175-1	ESRIP5	ESRIP5_HUMAN	EIF3E	Eukaryotic translation initiation factor 3 subunit E	1.0000	28.89	1	1	3
Q5175-2	ESRIJ25	ESRIJ25_HUMAN	EIF3E	Eukaryotic translation initiation factor 3 subunit E	1.0000	23.21	1	1	3
Q5175-3	ESRH55	ESRH55_HUMAN	EIF3E	Eukaryotic translation initiation factor 3 subunit E (Fragment)	1.0000	5.75	1	1	3
						HLVPLLEFLSVK	3	0.9994	3
Q5176-1	ESRIJ3	ESRIJ3_HUMAN	EIF3E	Eukaryotic translation initiation factor 3 subunit E	1.0000	41.33	2	2	4
Q5176-2	HOYBP5	HOYBP5_HUMAN	EIF3E	Eukaryotic translation initiation factor 3 subunit E (Fragment)	1.0000	41.89	2	2	4
						HLVPLLEFLSVK	3	0.9994	3
						LDLLSDTNMVDVDFAMDVYK	2	0.9754	1
Q5177-1	ESRIY1	ESRIY1_HUMAN	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory	1.0000	8.33	1	1	3
						VVIFQQEQENK	2	0.9989	3
Q5178-1	P11413	G6PD_HUMAN	G6PD	Glucose-6-phosphate 1-dehydrogenase	1.0000	12.82	6	6	7
Q5178-2	E7EM57	E7EM57_HUMAN	G6PD	Glucose-6-phosphate 1-dehydrogenase (Fragment)	1.0000	20.63	6	6	7
Q5178-3	E7EUI8	E7EUI8_HUMAN	G6PD	Glucose-6-phosphate 1-dehydrogenase (Fragment)	1.0000	19.53	6	6	7
Q5178-4	P11413-3	G6PD_HUMAN	G6PD	Isoform 3 of Glucose-6-phosphate 1-dehydrogenase	1.0000	12.11	6	6	7
Q5178-5	P11413-2	G6PD_HUMAN	G6PD	Isoform Long of Glucose-6-phosphate 1-dehydrogenase	1.0000	11.76	6	6	7
						DGLLPENTVGYAR	2	0.9596	1
						GGYDFEGIR	2	0.9995	2
						IDHYLKG	2	0.9762	1

						LFYALPPTVVEAVTK	2	0.8824	1
						LSNHISLSFR	3	0.9909	1
						LTVADIR	2	0.9977	1
Q5179-1	E7EMH5	E7EMH5_HUMAN	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing prote	0.9797	2.01	1	1	2
Q5179-2	E7EPL4	E7EPL4_HUMAN	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing prote	0.9797	1.84	1	1	2
Q5179-3	H3BN4D	H3BN4D_HUMAN	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing prote	0.9797	1.74	1	1	2
Q5179-4	H3BN21	H3BN21_HUMAN	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing prote	0.9797	1.84	1	1	2
Q5179-5	J3KNK7	J3KNK7_HUMAN	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing prote	0.9797	1.81	1	1	2
Q5179-6	Q6P996	PDXD1_HUMAN	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing prote	0.9797	1.78	1	1	2
						GEDVDQLVACIESK	2	0.9797	2
Q5180-1	E7EMM2	E7EMM2_HUMAN	AP3D1	AP-3 complex subunit delta	1.0000	1.83	2	2	3
Q5180-2	G5E988	G5E988_HUMAN	AP3D1	AP-3 complex subunit delta	1.0000	1.62	2	2	3
Q5180-3	O14617	AP3D1_HUMAN	AP3D1	AP-3 complex subunit delta-1	1.0000	1.56	2	2	3
Q5180-4	O14617-2	AP3D1_HUMAN	AP3D1	Isoform 2 of AP-3 complex subunit delta-1	1.0000	1.62	2	2	3
Q5180-5	O14617-3	AP3D1_HUMAN	AP3D1	Isoform 3 of AP-3 complex subunit delta-1	1.0000	1.83	2	2	3
Q5180-6	O14617-4	AP3D1_HUMAN	AP3D1	Isoform 4 of AP-3 complex subunit delta-1	1.0000	1.76	2	2	3
Q5180-7	O14617-5	AP3D1_HUMAN	AP3D1	Isoform 5 of AP-3 complex subunit delta-1	1.0000	1.48	2	2	3
						ASCLQLVK	2	0.9986	1
						LYASLQZK	2	0.9924	2
Q5181-1	E7EMM4	E7EMM4_HUMAN	ASAH1	Acid ceramidase	1.0000	27.57	8	8	15
Q5181-2	E7ERV9	E7ERV9_HUMAN	ASAH1	Acid ceramidase	1.0000	33.44	8	8	15
Q5181-3	Q13510	ASAH1_HUMAN	ASAH1	Acid ceramidase	1.0000	25.82	8	8	15
Q5181-4	Q13510-2	ASAH1_HUMAN	ASAH1	Isoform 2 of Acid ceramidase	1.0000	24.82	8	8	15
						ESLDVVELDAK	2	0.9992	1
						GQFETYLK	2	0.9932	1
						LPGLGNFGPFEEEMK	2	0.9996	3
						LTVYTTLIDVTK	2	0.9997	3
						NMINTFVPSGK	2	0.9753	1
						TSQENISFETMYDVLSTKPVLNK	3	0.9988	3
						WKHPFFLDR	3	0.9442	2
						WYVYQITNYDR	2	0.9938	1
Q5182-1	E7EM56	E7EM56_HUMAN	COMT	Catechol O-methyltransferase (Fragment)	1.0000	13.9	2	4	18
						LITIEINPDCAITOR	2	0.9997	7
						LITIEINPDCAITOR	3	0.9994	3
						YLPDTLLLEECGLLR	2	0.9997	5
						YLPDTLLLEECGLLR	3	0.9995	3
Q5183-1	P04070-2	PROC_HUMAN	PROC	Isoform 2 of Vitamin K-dependent protein C	1.0000	23.64	10	14	34
Q5183-2	P04070	PROC_HUMAN	PROC	Vitamin K-dependent protein C	1.0000	26.46	10	14	34
Q5183-3	E7EN06	E7EN06_HUMAN	PROC	Vitamin K-dependent protein C heavy chain	1.0000	24.65	10	14	34
						DTEDQEDQVDPR	2	0.9996	3
						ELNQAGQETLVGWGYHSSR	2	0.9997	3
						ELNQAGQETLVGWGYHSSR	3	0.985	1
						LGDLLLQCHPAVK	2	0.9996	4
						LGDLLLQCHPAVK	3	0.9972	1
						LGEYDLR	2	0.9988	2
						RGDSPWQVVLDSK	2	0.9992	2
						RGDSPWQVVLDSK	3	0.9995	3
						RGDSPWQVVLDSK	3	0.9984	2
						RWEKWELDLIK	2	0.9356	2
						RWEKWELDLIK	3	0.8513	1
						STTDNDIALHLAQPATLSQTIVPICLPDPSGLAER	3	0.9991	6
						TFVLNFIK	2	0.9997	2
						WELDLIK	2	0.9926	2
Q5184-1	P61313	RL15_HUMAN	RPL15	60S ribosomal protein L15	1.0000	12.75	2	2	4
Q5184-2	E7ENU7	E7ENU7_HUMAN	RPL15	Ribosomal protein L15 (Fragment)	1.0000	14.86	2	2	4
Q5184-3	E7EQV9	E7EQV9_HUMAN	RPL15	Ribosomal protein L15 (Fragment)	1.0000	14.94	2	2	4
						FFEVILPPFAK	3	0.9992	2
						VLNSYWGVEDSTYK	2	0.9996	2
Q5185-1	E7EP32	E7EP32_HUMAN	GNB2	Guanine nucleotide-binding protein G(i1)/G(s)/G(t) subunit b	1.0000	33.78	6	6	8
Q5185-2	P62879	GNB2_HUMAN	GNB2	Guanine nucleotide-binding protein G(i1)/G(s)/G(t) subunit b	1.0000	29.41	6	6	8
						ADQELMYSHDNIICGITSVAFSR	3	0.9995	3
						ELPGHTGYLSCCR	2	0.9377	1
						LLAGYDFDNCNIWDAMK	2	0.9976	1
						LLVSASQDGK	2	0.9815	1
						TFVSGACDASIK	2	0.9995	1
						VSLGVTDDGMVATGSGWDSFLK	2	0.9993	1
Q5186-1	E7EPB3	E7EPB3_HUMAN	RPL14	60S ribosomal protein L14	1.0000	18.55	2	3	5
Q5186-2	P50914	RL14_HUMAN	RPL14	60S ribosomal protein L14	1.0000	10.7	2	3	5
						ALVDGPRCTQYR	2	0.9799	2
						LVAIVDIDONR	2	0.9997	2
						LVAIVDIDONR	3	0.9493	1
Q5187-1	E7EPC6	E7EPC6_HUMAN	CD44	CD44 antigen	0.9826	1.68	1	1	2
Q5187-2	HOYD13	HOYD13_HUMAN	CD44	CD44 antigen	0.9826	5.83	1	1	2
Q5187-3	P16070	CD44_HUMAN	CD44	CD44 antigen	0.9826	1.62	1	1	2
Q5187-4	HOY2P0	HOY2P0_HUMAN	CD44	CD44 antigen (Fragment)	0.9826	4.18	1	1	2
Q5187-5	HOY5E4	HOY5E4_HUMAN	CD44	CD44 antigen (Fragment)	0.9826	4.08	1	1	2
Q5187-6	HOYCV9	HOYCV9_HUMAN	CD44	CD44 antigen (Fragment)	0.9826	4.82	1	1	2
Q5187-7	HOYD17	HOYD17_HUMAN	CD44	CD44 antigen (Fragment)	0.9826	5.24	1	1	2
Q5187-8	HOYDW7	HOYDW7_HUMAN	CD44	CD44 antigen (Fragment)	0.9826	5	1	1	2
Q5187-9	HOYDX6	HOYDX6_HUMAN	CD44	CD44 antigen (Fragment)	0.9826	6.63	1	1	2
Q5187-10	P16070-10	CD44_HUMAN	CD44	Isoform 10 of CD44 antigen	0.9826	2.43	1	1	2
Q5187-11	P16070-11	CD44_HUMAN	CD44	Isoform 11 of CD44 antigen	0.9826	2.8	1	1	2
Q5187-12	P16070-12	CD44_HUMAN	CD44	Isoform 12 of CD44 antigen	0.9826	3.32	1	1	2
Q5187-13	P16070-13	CD44_HUMAN	CD44	Isoform 13 of CD44 antigen	0.9826	2.82	1	1	2
Q5187-14	P16070-14	CD44_HUMAN	CD44	Isoform 14 of CD44 antigen	0.9826	3.03	1	1	2
Q5187-15	P16070-15	CD44_HUMAN	CD44	Isoform 15 of CD44 antigen	0.9826	4.08	1	1	2
Q5187-16	P16070-16	CD44_HUMAN	CD44	Isoform 16 of CD44 antigen	0.9826	1.8	1	1	2
Q5187-17	P16070-17	CD44_HUMAN	CD44	Isoform 17 of CD44 antigen	0.9826	1.74	1	1	2
Q5187-18	P16070-18	CD44_HUMAN	CD44	Isoform 18 of CD44 antigen	0.9826	3.53	1	1	2
Q5187-19	P16070-3	CD44_HUMAN	CD44	Isoform 3 of CD44 antigen	0.9826	1.69	1	1	2
Q5187-20	P16070-4	CD44_HUMAN	CD44	Isoform 4 of CD44 antigen	0.9826	1.72	1	1	2
Q5187-21	P16070-5	CD44_HUMAN	CD44	Isoform 5 of CD44 antigen	0.9826	1.63	1	1	2
Q5187-22	P16070-6	CD44_HUMAN	CD44	Isoform 6 of CD44 antigen	0.9826	1.72	1	1	2
Q5187-23	P16070-7	CD44_HUMAN	CD44	Isoform 7 of CD44 antigen	0.9826	1.68	1	1	2
Q5187-24	P16070-8	CD44_HUMAN	CD44	Isoform 8 of CD44 antigen	0.9826	1.78	1	1	2
Q5187-25	P16070-9	CD44_HUMAN	CD44	Isoform 9 of CD44 antigen	0.9826	1.78	1	1	2
						YGFIEGHVPIPR	3	0.9826	2
Q5188-1	E7EQ64	E7EQ64_HUMAN	PRSS1	Trypsin-1	0.9359	3.83	1	1	1
Q5188-2	P07477	TRY1_HUMAN	PRSS1	Trypsin-1	0.9359	4.05	1	1	1
Q5188-3	HOY8D1	HOY8D1_HUMAN	PRSS1	Trypsin-1 (Fragment)	0.9359	7.04	1	1	1
						TLNNDIMLIK	2	0.9359	1
Q5189-1	E7EQB2	E7EQB2_HUMAN	LTF	Kaliocin-1 (Fragment)	1.0000	55.32	30	35	79
Q5189-2	P02788	TRFL_HUMAN	LTF	Lactotransferrin	1.0000	54.23	30	35	79
						ADAVTLDDGFIYEAGLAPYK	2	0.9937	1
						CAFSSQEPYFSYGAFK	2	0.9996	4
						CGLVPLVAENYK	2	0.9991	1
						CLAENAGDAVAVK	2	0.9995	3
						CSTSLPEACEFLK	2	0.9869	2
						DEYFSQSCAPSGSDR	2	0.9934	2
						DGAGDVAFIR	2	0.9985	2
						DGAGDVAFIRE	2	0.8743	2
						DLLFKDSAGFSR	3	0.8982	1
						DSPIQCIQIAENR	2	0.999	4
						DSPIQCIQIAENR	3	0.8833	1
						ESTVFEDLSDEARDEVELLCPDNTK	3	0.9601	2
						GEADMSLDGGVYTAGK	2	0.9996	3
						GGSFQNLQGLK	2	0.999	3
						IDSGLYLGSGYFTAIQNLK	2	0.9996	3
						IDSGLYLGSGYFTAIQNLK	3	0.9962	3
						KCNQWSGLSGSYTCSSASTTEOCIALVLK	3	0.9633	1
						KGGSFQNLQGLK	2	0.9974	3
						KGGSFQNLQGLK	3	0.9823	1
						LADFALLCLDGK	2	0.9995	3

						LLFNDNTECLAR	2	0.9723	2
						LRPVAEEVGTGR	2	0.999	2
						LRPVAEEVGTGR	3	0.9989	1
						NLLFNDNTECLAR	2	0.9994	4
						SDTSLTWNSVK	2	0.9971	2
						SNLCALCIGDEGENK	2	0.9996	2
						SQSSSDPINCVDPPVGGVLAIVAVR	3	0.9986	4
						SVQWCAVSQPEATK	2	0.9996	2
						THYYAVAVVK	2	0.9902	1
						THYYAVAVVK	3	0.9251	1
						TLDDGGFIYEAGLAPYK	2	0.9876	3
						VVWCAVGEQELR	2	0.9995	4
						VVWCAVGEQELRK	2	0.999	2
						YLGPOYVAGITNLK	2	0.9991	2
						YGYGTGAFR	2	0.9983	2
Q5190-1	P60842	IF4A1_HUMAN	EIF4A1	Eukaryotic initiation factor 4A-I	1.0000	7.39	2	3	3
Q5190-2	E7EQG2	E7EQG2_HUMAN	EIF4A2	Eukaryotic initiation factor 4A-II	1.0000	8.29	2	3	3
Q5190-3	Q14240	IF4A2_HUMAN	EIF4A2	Eukaryotic initiation factor 4A-II	1.0000	7.37	2	3	3
Q5190-4	Q14240-2	IF4A2_HUMAN	EIF4A2	Isoform 2 of Eukaryotic initiation factor 4A-II	1.0000	7.35	2	3	3
						GIYAYGEKPSAIQQR	2	0.9996	1
						GIYAYGEKPSAIQQR	3	0.9939	1
						GYDVIAQAQSGTGK	2	0.9982	1
Q5191-1	E7EQI7	E7EQI7_HUMAN	KIAA0196	WASH complex subunit strumpellin	0.9977	1.48	1	1	2
Q5191-2	Q12768	STRUM_HUMAN	KIAA0196	WASH complex subunit strumpellin	0.9977	1.29	1	1	2
						SFEYIQDYVNIYGLK	2	0.9902	2
Q5192-1	E7EQR4	E7EQR4_HUMAN	EZR	Ezrin	1.0000	15.52	7	7	14
Q5192-2	P15311	EZR_HUMAN	EZR	Ezrin	1.0000	14.68	7	7	14
						AKFYFEDVAELIQDITQK	3	0.9977	3
						APDFVYAPR	2	0.9896	1
						IALLLEAR	2	0.9929	1
						IAQDLEMYGINIFYEIK	2	0.9996	3
						IGFPWSEIR	2	0.9994	2
						IQVWMAEHR	2	0.9996	2
						SQEQLAAELAYTAK	2	0.9996	2
Q5193-1	E7EQR6	E7EQR6_HUMAN	TCP1	T-complex protein 1 subunit alpha	1.0000	7.23	3	3	5
Q5193-2	F5H282	F5H282_HUMAN	TCP1	T-complex protein 1 subunit alpha	1.0000	8.73	3	3	5
						EQIAIAEFAR	2	0.9985	2
						FATEAAITLR	2	0.9996	2
						TSASILRL	2	0.9936	1
Q5194-1	E7ER27	E7ER27_HUMAN	HSD17B4	Peroxisomal multifunctional enzyme type 2	1.0000	4.4	2	2	2
Q5194-2	P51659	DHB4_HUMAN	HSD17B4	Peroxisomal multifunctional enzyme type 2	1.0000	2.99	2	2	2
						AYALAFAR	2	0.9946	1
Q5195-1	E7ER44	E7ER44_HUMAN	LTF	Kallicrein-1	1.0000	50.28	29	4	78
						ADAVTLDDGGFIYEAGLAPYK	2	0.9937	1
						CAFSSQEPYFSYGAFK	2	0.9996	4
						CGLVPVLAENYK	2	0.9991	1
						CLAENAGDVAEVK	2	0.9995	3
						CSTSPILLEACEFLR	2	0.9869	2
						DEYFSQSCAPGSDPR	2	0.9934	2
						DGAGDVAFIR	2	0.9985	2
						DGAGDVAFIRE	2	0.8743	2
						DLLFKDSAIGFSR	3	0.8982	1
						DSPIQCIQIAENR	2	0.999	4
						DSPIQCIQIAENR	3	0.8833	1
						ESTVFELSDAEAREDEYELLCPDNR	3	0.9601	2
						GEADAMSDDGGVYTAGK	2	0.9996	3
						GGSFQNLQGLK	2	0.999	3
						IDSGLYLGSYFTAQNLRL	2	0.9996	3
						IDSGLYLGSYFTAQNLRL	3	0.9962	3
						KGGSFQNLQGLK	2	0.9974	3
						KGGSFQNLQGLK	3	0.9823	1
						LADFALLCLDGK	2	0.9995	3
						LLFNDNTECLAR	2	0.9723	2
						LRPVAEEVGTGR	2	0.999	2
						LRPVAEEVGTGR	3	0.9989	1
						NLLFNDNTECLAR	2	0.9994	4
						SDTSLTWNSVK	2	0.9971	2
						SNLCALCIGDEGENK	2	0.9996	2
						SQSSSDPINCVDPPVGGVLAIVAVR	3	0.9986	4
						SVQWCAVSQPEATK	2	0.9996	2
						THYYAVAVVK	2	0.9902	1
						THYYAVAVVK	3	0.9251	1
						TLDDGGFIYEAGLAPYK	2	0.9876	3
						VVWCAVGEQELR	2	0.9995	4
						VVWCAVGEQELRK	2	0.999	2
						YLGPOYVAGITNLK	2	0.9991	2
						YGYGTGAFR	2	0.9983	2
Q5196-1	E9PFL9	E9PFL9_HUMAN	SSB	Lupus La protein	1.0000	22.39	2	3	6
Q5196-2	P05455	LA_HUMAN	SSB	Lupus La protein	1.0000	7.35	2	3	6
Q5196-3	E7ERC4	E7ERC4_HUMAN	SSB	Lupus La protein (Fragment)	1.0000	16.3	2	3	6
						ICHOIEYFGDFNLRL	2	0.9695	1
						ICHOIEYFGDFNLRL	3	0.9717	2
						LTFDNNVIVEALSK	2	0.9996	3
Q5197-1	P15531-2	NDKA_HUMAN	NME1	Isoform 2 of Nucleoside diphosphate kinase A	0.9508	5.08	1	1	1
Q5197-2	E7ERL0	E7ERL0_HUMAN	NME1	Nucleoside diphosphate kinase A	0.9508	6.47	1	1	1
Q5197-3	P15531	NDKA_HUMAN	NME1	Nucleoside diphosphate kinase A	0.9508	5.92	1	1	1
Q5197-4	F6XY72	F6XY72_HUMAN	NME1-NME2	Nucleoside diphosphate kinase	0.9508	11.69	1	1	1
Q5197-5	Q32Q12	Q32Q12_HUMAN	NME1-NME2	Nucleoside diphosphate kinase	0.9508	3.08	1	1	1
Q5197-6	P22392-2	NDKB_HUMAN	NME2	Isoform 3 of Nucleoside diphosphate kinase B	0.9508	3.37	1	1	1
Q5197-7	J3KPD9	J3KPD9_HUMAN	NME2	Nucleoside diphosphate kinase B	0.9508	4.57	1	1	1
Q5197-8	P22392	NDKB_HUMAN	NME2	Nucleoside diphosphate kinase B	0.9508	5.92	1	1	1
Q5197-9	O60361	NDKB_HUMAN	NME2P1	Putative nucleoside diphosphate kinase	0.9508	6.57	1	1	1
Q5198-1	E7ES19	E7ES19_HUMAN	THBS4	Thrombospondin-4	1.0000	7.01	3	3	5
Q5198-2	P35443	TPS4_HUMAN	THBS4	Thrombospondin-4	1.0000	6.35	3	3	5
						DGIGDECDDDDNDGIDLVPPGPONCR	3	0.8176	1
						DVIDISYDPEELPCASR	2	0.9994	3
						PELNPCSVNAQCIEER	2	0.8175	1
Q5199-1	F5GYB5	F5GYB5_HUMAN	RAP1B	Ras-related protein Rap-1b	1.0000	8.09	1	1	1
Q5199-2	F5H7Y6	F5H7Y6_HUMAN	RAP1B	Ras-related protein Rap-1b	1.0000	6.15	1	1	1
Q5199-3	E7ESV4	E7ESV4_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	7.01	1	1	1
Q5199-4	F5GWU8	F5GWU8_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	12.64	1	1	1
Q5199-5	F5GX62	F5GX62_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	7.91	1	1	1
Q5199-6	F5GYH7	F5GYH7_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	20.75	1	1	1
Q5199-7	F5H0D4	F5H0D4_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	8.66	1	1	1
Q5199-8	F5H077	F5H077_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	13.1	1	1	1
Q5199-9	F5H0B7	F5H0B7_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	11.22	1	1	1
Q5199-10	F5H491	F5H491_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	11.83	1	1	1
Q5199-11	F5H4H0	F5H4H0_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	22.92	1	1	1
Q5199-12	F5H500	F5H500_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	10.89	1	1	1
Q5199-13	F5H6R7	F5H6R7_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	9.02	1	1	1
Q5199-14	F8WBC0	F8WBC0_HUMAN	RAP1B	Ras-related protein Rap-1b (Fragment)	1.0000	34.38	1	1	1
						LVLVLSGGVGK	2	0.9992	1
Q5200-1	P62136-2	PPP1A_HUMAN	PPP1CA	Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha	1.0000	4.99	1	1	3
Q5200-2	E9PMD7	E9PMD7_HUMAN	PPP1CA	Serine/threonine-protein phosphatase (Fragment)	1.0000	6.72	1	1	3
Q5200-3	P62136	PPP1A_HUMAN	PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic su	1.0000	5.15	1	1	3
Q5200-4	F5H037	F5H037_HUMAN	PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic su	1.0000	9.5	1	1	3
Q5200-5	F5H1L6	F5H1L6_HUMAN	PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic su	1.0000	10.06	1	1	3
Q5200-6	E7ETD8	E7ETD8_HUMAN	PPP1CB	Serine/threonine-protein phosphatase (Fragment)	1.0000	10.06	1	1	3
Q5200-7	F8WE71	F8WE71_HUMAN	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic su	1.0000	26.56	1	1	3
Q5200-8	P36873-2	PPP1G_HUMAN	PPP1CC	Isoform Gamma-2 of Serine/threonine-protein phosphatase	1.0000	5.04	1	1	3
Q5200-9	F8VR82	F8VR82_HUMAN	PPP1CC	Serine/threonine-protein phosphatase	1.0000	6.3	1	1	3

Q5200-10	F8VYE8	F8VYE8_HUMAN	PPP1CC	Serine/threonine-protein phosphatase	1.0000	5.59	1	1	3
Q5200-11	F8W0W8	F8W0W8_HUMAN	PPP1CC	Serine/threonine-protein phosphatase	1.0000	5.12	1	1	3
Q5200-12	P36873	PP1G_HUMAN	PPP1CC	Serine/threonine-protein phosphatase PP1-gamma catalytic	1.0000	5.26	1	1	3
Q5201-1	P62820-3	RAB1A_HUMAN	RAB1A	Isoform 3 of Ras-related protein Rab-1A	1.0000	EIFLSQPILLEEAPLK	2	0.9997	3
Q5201-2	E7ETK2	E7ETK2_HUMAN	RAB1A	Ras-related protein Rab-1A	1.0000	23.26	2	2	4
						23.26	2	2	4
						FADDYTESVSTIGVDFK	2	0.9994	2
						LLIGDSGVGK	2	0.985	2
Q5202-1	E7ETK5	E7ETK5_HUMAN	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)	1.0000	12.54	3	4	6
						HGFCGPIITDGR	2	0.9992	1
						LVGIISR	2	0.996	1
						REDLVVAPAGITLK	2	0.9996	2
						REDLVVAPAGITLK	3	0.998	2
Q5203-1	P06681	CO2_HUMAN	C2	Complement C2	1.0000	1.35	1	1	2
						CPAPVSFENGITPR	2	0.9991	2
Q5204-1	P50395-2	GDI8_HUMAN	GDI2	Isoform 2 of Rab GDP dissociation inhibitor beta	1.0000	17.5	6	7	10
Q5204-2	E7EU23	E7EU23_HUMAN	GDI2	Rab GDP dissociation inhibitor beta	1.0000	15.59	6	7	10
Q5204-3	P50395	GDI8_HUMAN	GDI2	Rab GDP dissociation inhibitor beta	1.0000	15.73	6	7	10
						DLGTESQIFSR	2	0.9995	2
						FDLGGQVIDFTGHALALYR	3	0.9737	1
						FVSIQDLVPK	2	0.9936	1
						KFDLGGQVIDFTGHALALYR	3	0.9996	3
						KFDLGGQVIDFTGHALALYR	4	0.9903	1
						LYSESLAR	2	0.976	1
						SPVLYPLVGLGELPQGFAR	2	0.9995	1
Q5205-1	Q16851-2	UGPA_HUMAN	UGP2	Isoform 2 of UTP--glucose-1-phosphate uridylyltransferase	0.9997	7.85	3	3	3
Q5205-2	E7EUC7	E7EUC7_HUMAN	UGP2	UTP--glucose-1-phosphate uridylyltransferase	0.9997	7.54	3	3	3
Q5205-3	Q16851	UGPA_HUMAN	UGP2	UTP--glucose-1-phosphate uridylyltransferase	0.9997	7.68	3	3	3
						LVEIAQVPK	2	0.9953	1
						NENTFLDLTVQQIEHLNK	3	0.982	1
						SPFNSLGINVPR	2	0.9063	1
Q5206-1	E7EUT5	E7EUT5_HUMAN	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	1.0000	66.92	14	18	69
						AGAEEYVVESTGVFTTMEK	2	0.8445	1
						GALQNIIPASTGAOK	2	0.9997	3
						GILGYTEHQVSSDFNSDTHSTFDAGAGIALNDHFVK	4	0.9881	3
						IISNASCTTNCLAPLAK	2	0.9997	4
						LEKPAKYDDIK	2	0.9917	3
						LEKPAKYDDIKK	2	0.999	4
						LISWYDNEFGYSNR	2	0.9998	9
						LISWYDNEFGYSNR	3	0.9993	3
						LTGMARVPTANVSVDLTCR	3	0.9994	3
						SWYDNEFGYSNR	2	0.9964	3
						VIHONFGIVEGLMTTV	2	0.9446	1
						VIHONFGIVEGLMTTVHATATQK	3	0.9996	11
						VIHONFGIVEGLMTTVHATATQK	4	0.9881	4
						VPTANVSVDLTCR	2	0.9998	5
						VVDLMAHMASKE	2	0.9997	2
						VVDLMAHMASKE	3	0.9841	2
						WGDAGAEYVVESTGVFTTMEK	2	0.9997	5
						WGDAGAEYVVESTGVFTTMEK	3	0.9996	3
Q5207-1	Q9UM54-1	MYO6_HUMAN	MYO6	Isoform 1 of Unconventional myosin-VI	1.0000	6.77	5	6	8
Q5207-2	Q9UM54-2	MYO6_HUMAN	MYO6	Isoform 2 of Unconventional myosin-VI	1.0000	6.89	5	6	8
Q5207-3	Q9UM54-4	MYO6_HUMAN	MYO6	Isoform 4 of Unconventional myosin-VI	1.0000	6.77	5	6	8
Q5207-4	Q9UM54-5	MYO6_HUMAN	MYO6	Isoform 5 of Unconventional myosin-VI	1.0000	6.94	5	6	8
Q5207-5	Q9UM54-6	MYO6_HUMAN	MYO6	Isoform 6 of Unconventional myosin-VI	1.0000	6.77	5	6	8
Q5207-6	E7EW20	E7EW20_HUMAN	MYO6	Unconventional myosin-VI	1.0000	6.77	5	6	8
Q5207-7	Q9UM54	MYO6_HUMAN	MYO6	Unconventional myosin-VI	1.0000	6.72	5	6	8
						IAQSEAEISDEAQADLALR	2	0.9996	2
						LCAGASEIDREK	2	0.9782	2
						MSQSIIVSGESGAGKNTXK	2	0.9977	1
						SAQSLYCAELGLDQDDLR	2	0.9989	1
						SAQSLYCAELGLDQDDLR	3	0.9987	1
						YLTESYGTGQIDDDR	2	0.9989	1
Q5208-1	E7EW44	E7EW44_HUMAN	CORO1B	Coronin	1.0000	8.3	2	2	4
Q5208-2	F5H0D2	F5H0D2_HUMAN	CORO1B	Coronin	1.0000	13.11	2	2	4
Q5208-3	F5H390	F5H390_HUMAN	CORO1B	Coronin	1.0000	8.51	2	2	4
						VGIIAHWPTAR	3	0.9992	2
						VTWDSTFCVNPXK	2	0.9996	2
Q5209-1	E7EWT1	E7EWT1_HUMAN	DDOST	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	1.0000	2.63	1	1	2
						TLVLNLNLNVR	2	0.9994	2
Q5210-1	E9PAV3-2	NACAM_HUMAN	NACA	Isoform 2 of Nascent polypeptide-associated complex subunit alpha	1.0000	2.92	2	2	4
Q5210-2	Q13765	NACA_HUMAN	NACA	Nascent polypeptide-associated complex subunit alpha	1.0000	12.56	2	2	4
Q5210-3	E9PAV3	NACAM_HUMAN	NACA	Nascent polypeptide-associated complex subunit alpha, muscle	1.0000	1.3	2	2	4
Q5210-4	F8VZJ2	F8VZJ2_HUMAN	NACA	Nascent polypeptide-associated complex subunit alpha, muscle	1.0000	19.85	2	2	4
Q5210-5	F8VNW4	F8VNW4_HUMAN	NACA	Nascent polypeptide-associated complex subunit alpha, muscle	1.0000	18.24	2	2	4
Q5210-6	F8W0W4	F8W0W4_HUMAN	NACA	Nascent polypeptide-associated complex subunit alpha, muscle	1.0000	13.64	2	2	4
Q5210-7	F8W1N5	F8W1N5_HUMAN	NACA	Nascent polypeptide-associated complex subunit alpha, muscle	1.0000	38.03	2	2	4
Q5210-8	H0YHX9	H0YHX9_HUMAN	NACA	Nascent polypeptide-associated complex subunit alpha, muscle	1.0000	12.68	2	2	4
						NILFVITKPDVYK	2	0.9979	2
						SPASDTYVGEAK	2	0.9997	2
Q5211-1	E9PB90	E9PB90_HUMAN	HK2	Hexokinase-2	0.9999	2.47	2	2	2
Q5211-2	P52789	H0K2_HUMAN	HK2	Hexokinase-2	0.9999	2.4	2	2	2
						GAALITAVACR	2	0.9987	1
						NVELVEEGEGR	2	0.9554	1
Q5212-1	E9PBC5	E9PBC5_HUMAN	KLKB1	Plasma kallikrein heavy chain	1.0000	2.54	1	1	2
						IAYGTQSSGYSLR	2	0.9994	2
Q5213-1	E9PBW4	E9PBW4_HUMAN	HGB2	Hemoglobin subunit gamma-2	1.0000	16.06	2	2	3
						EFTPEVQASWQK	2	0.9978	2
						VLTSLGDAIK	2	0.9761	1
Q5214-1	E9PB22	E9PB22_HUMAN	HPGD	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	1.0000	30.68	5	5	10
Q5214-2	P15428-4	PGDH_HUMAN	HPGD	Isoform 4 of 15-hydroxyprostaglandin dehydrogenase [NAD(+)]	1.0000	37.76	5	5	10
						AALDEQFEPQK	2	0.9997	4
						AFAEALLLK	2	0.9996	2
						LDLVNNAAGVNNNEK	2	0.9997	2
						VALVTGAAGIGIR	2	0.9997	1
						VVDHFGK	2	0.9946	1
Q5215-1	P24821-2	TENA_HUMAN	TNC	Isoform 2 of Tenascin	0.9992	0.69	1	1	2
Q5215-2	P24821-3	TENA_HUMAN	TNC	Isoform 3 of Tenascin	0.9992	0.65	1	1	2
Q5215-3	P24821-4	TENA_HUMAN	TNC	Isoform 4 of Tenascin	0.9992	0.57	1	1	2
Q5215-4	P24821-5	TENA_HUMAN	TNC	Isoform 5 of Tenascin	0.9992	0.73	1	1	2
Q5215-5	P24821-6	TENA_HUMAN	TNC	Isoform 6 of Tenascin	0.9992	0.77	1	1	2
Q5215-6	E9PC84	E9PC84_HUMAN	TNC	Tenascin	0.9992	0.62	1	1	2
Q5215-7	F5H7V9	F5H7V9_HUMAN	TNC	Tenascin	0.9992	0.65	1	1	2
Q5215-8	J3QSU6	J3QSU6_HUMAN	TNC	Tenascin	0.9992	0.59	1	1	2
Q5215-9	P24821	TENA_HUMAN	TNC	Tenascin	0.9992	0.55	1	1	2
						LEELLENLVSSLR	2	0.9987	2
Q5216-1	E9PCY7	E9PCY7_HUMAN	HNRNP1	Heterogeneous nuclear ribonucleoprotein H	1.0000	6.29	2	2	4
Q5216-2	G8LB6	G8LB6_HUMAN	HNRNP1	Heterogeneous nuclear ribonucleoprotein H	1.0000	5.72	2	2	4
Q5216-3	P31943	HNRH1_HUMAN	HNRNP1	Heterogeneous nuclear ribonucleoprotein H	1.0000	6.01	2	2	4
Q5216-4	H0YB39	H0YB39_HUMAN	HNRNP1	Heterogeneous nuclear ribonucleoprotein H (Fragment)	1.0000	9.75	2	2	4
Q5216-5	P55795	HNRH2_HUMAN	HNRNP2	Heterogeneous nuclear ribonucleoprotein H2	1.0000	6.01	2	2	4
						STGEAFVQFASQIEIAEK	2	0.9992	2
						VHIEIGPDGR	2	0.9986	2
Q5217-1	E9PEW8	E9PEW8_HUMAN	HBD	Hemoglobin subunit delta (Fragment)	1.0000	14.42	1	1	1
						SELHCDKLHVDPENF	2	0.8135	1
Q5218-1	F8VT20	F8VT20_HUMAN	PCBP2	Poly(rC)-binding protein 2 (Fragment)	0.9995	17.19	1	1	2
Q5218-2	P57721-2	PCBP3_HUMAN	PCBP3	Isoform 2 of Poly(rC)-binding protein 3	0.9995	3.19	1	1	2
Q5218-3	P57721-3	PCBP3_HUMAN	PCBP3	Isoform 3 of Poly(rC)-binding protein 3	0.9995	3.18	1	1	2
Q5218-4	P57721-4	PCBP3_HUMAN	PCBP3	Isoform 4 of Poly(rC)-binding protein 3	0.9995	2.97	1	1	2
Q5218-5	P57721-5	PCBP3_HUMAN	PCBP3	Isoform 5 of Poly(rC)-binding protein 3	0.9995	3.13	1	1	2
Q5218-6	E9PF8	E9PF8_HUMAN	PCBP3	Poly(rC)-binding protein 3	0.9995	3.05	1	1	2
Q5218-7	P57721	PCBP3_HUMAN	PCBP3	Poly(rC)-binding protein 3	0.9995	2.96	1	1	2
Q5218-8	J3QT27	J3QT27_HUMAN	PCBP3	Poly(rC)-binding protein 3 (Fragment)	0.9995	3.42	1	1	2

						INISEGNCPER	2	0.9946	2
QS219-1	E9PF22	E9PF22_HUMAN	CP	Ceruloplasmin	1.0000	9.94	9	9	13
QS219-2	P0D450	CERU_HUMAN	CP	Ceruloplasmin	1.0000	8.83	9	9	13
						ALYLQYTDETR	2	0.9993	2
						DIASGLGLIICK	2	0.9676	1
						EVGPTNADVPCLAK	2	0.9281	1
						EYTDASTFNR	2	0.8086	1
						EYTDASTFNRK	2	0.9964	2
						GAYPLSIEPIGVR	2	0.9988	2
						QSEDSTFYLGER	2	0.9816	2
						RQSEDSTFYLGER	2	0.8999	1
						TTIEKPWWLGLGLPIIK	3	0.8493	1
QS220-1	E9PG40	E9PG40_HUMAN	APP	Gamma-secretase C-terminal fragment 59	1.0000	20.45	11	11	22
						CAPFYFGCGGNR	2	0.9997	2
						CLVGEFVSALLVPDKCK	3	0.9913	1
						EVCSEQAETGPCR	2	0.9997	3
						ISYGNDALMPSLTETK	2	0.9989	2
						LALENVITALQAVPPRRP	3	0.9754	1
						QQLVETHMAR	2	0.9832	1
						SQVMTHLR	2	0.9979	2
						STNLHDYGMLLPCGIDKFR	3	0.9475	1
						THPHFVIPIYR	3	0.9994	3
						VESLEQEAANER	2	0.9975	2
						WYFDVTEGK	2	0.9997	4
QS221-1	E9PGP2	E9PGP2_HUMAN	F11	Coagulation factor XI	1.0000	22.16	9	9	15
QS221-2	P03951	FA11_HUMAN	F11	Coagulation factor XI	1.0000	20.32	9	9	15
QS221-3	P03951-2	FA11_HUMAN	F11	Isoform 2 of Coagulation factor XI	1.0000	22.24	9	9	15
						CLLFTFTAESPEDPTR	2	0.9997	3
						DTCFEGGDITTVTPSAK	2	0.9997	2
						ERPQVYTNVVEYVDWILEK	2	0.9952	3
						GGISGYTLR	2	0.9935	1
						HNEVWMLVIGITSWEGCAQR	3	0.9979	2
						NVYTDCWYTWGWIYR	2	0.997	1
						SCALSNLACIR	2	0.9262	1
						WFTCVLK	2	0.974	1
						YCVQVCTHYPR	2	0.9994	1
QS222-1	E9PGX9	E9PGX9_HUMAN	S5B	Lupus La protein (Fragment)	1.0000	11.67	1	1	3
						LTTDFNVIVEALSK	2	0.9996	3
QS223-1	E9PHH3	E9PHH3_HUMAN	SDC1	Syndecan-1	1.0000	10.06	3	4	8
QS223-2	P18827	SDC1_HUMAN	SDC1	Syndecan-1	1.0000	5.48	3	4	8
QS223-3	H7C1K4	H7C1K4_HUMAN	SDC1	Syndecan-1 (Fragment)	1.0000	7.91	3	4	8
						EGEAVVLPEVEPGLTAR	2	0.9997	5
						EGEAVVLPEVEPGLTAR	3	0.9862	1
						PEVEPGLTAR	2	0.9948	1
						VLPEVEPGLTAR	2	0.8542	1
QS224-1	E9PHK0	E9PHK0_HUMAN	CLEC3B	Tetranectin	1.0000	7.5	1	2	3
QS224-2	P05452	TETN_HUMAN	CLEC3B	Tetranectin	1.0000	5.94	1	2	3
						TFHEASEDCISR	2	0.9993	2
						TFHEASEDCISR	3	0.956	1
QS225-1	E9PHT9	E9PHT9_HUMAN	ANXA5	Annexin	0.9765	9.82	1	1	1
QS225-2	P08758	ANXA5_HUMAN	ANXA5	Annexin A5	0.9765	5	1	1	1
						GLGTDEESILTLTSTR	2	0.9765	1
QS226-1	E9PLE5	E9PLE5_HUMAN	RIC8A	Synembryn-A	1.0000	36.54	1	1	3
QS226-2	E9PI04	E9PI04_HUMAN	RIC8A	Synembryn-A (Fragment)	1.0000	12.84	1	1	3
						AVAEAVETGEEDVIMEALR	2	0.9997	3
QS227-1	E9PIF4	E9PIF4_HUMAN	NEU1	Sialidase-1	0.9998	7.12	2	2	2
QS227-2	Q99519	NEU1_HUMAN	NEU1	Sialidase-1	0.9998	4.58	2	2	2
						GTLLAFAEAR	2	0.9936	1
						IFLUTATPR	2	0.9684	1
QS228-1	E9PPV6	E9PPV6_HUMAN	SERPINH1	Serpin H1	0.9929	8.95	2	2	2
QS228-2	P50454	SERPH_HUMAN	SERPINH1	Serpin H1	0.9929	6.94	2	2	2
QS228-3	E9PIG2	E9PIG2_HUMAN	SERPINH1	Serpin H1 (Fragment)	0.9929	17.58	2	2	2
QS228-4	E9PIH8	E9PIH8_HUMAN	SERPINH1	Serpin H1 (Fragment)	0.9929	19.33	2	2	2
QS228-5	E9PK86	E9PK86_HUMAN	SERPINH1	Serpin H1 (Fragment)	0.9929	11.74	2	2	2
QS228-6	E9PMI5	E9PMI5_HUMAN	SERPINH1	Serpin H1 (Fragment)	0.9929	11.65	2	2	2
QS228-7	E9PNX1	E9PNX1_HUMAN	SERPINH1	Serpin H1 (Fragment)	0.9929	14.29	2	2	2
QS228-8	E9PR70	E9PR70_HUMAN	SERPINH1	Serpin H1 (Fragment)	0.9929	9.83	2	2	2
QS228-9	E9PRS3	E9PRS3_HUMAN	SERPINH1	Serpin H1 (Fragment)	0.9929	17.47	2	2	2
						LYGPSVSFADDVFR	2	0.9127	1
						SAGLAFSLVQAMAK	2	0.9188	1
QS229-1	E9PIT3	E9PIT3_HUMAN	F2	Thrombin light chain	1.0000	34.65	29	32	161
						ACLEGNCAEGLGTNYR	2	0.9983	3
						ANTFLEVR	2	0.9055	1
						CYTTPDPTVR	2	0.9121	1
						DKLAACLEGNCAEGLGTNYR	3	0.9995	16
						ELLESYIDGR	2	0.9997	8
						ETWTANVGK	2	0.995	1
						HQDFNSAVQLVENFCR	3	0.9997	4
						KSQELLCGASUSDR	2	0.9997	6
						KSQPELLCGASUSDR	3	0.9997	5
						LAACLEGNCAEGLGTNYR	2	0.9997	12
						LAVTTNGLPCLAWASQAQK	2	0.9997	4
						LAVTTNGLPCLAWASQAQK	3	0.9997	7
						LEGNCAEGLGTNYR	2	0.9988	4
						NPDSTTGPWCYTTPDPTVR	2	0.9983	3
						NPDSSTTGPWCYTTPDPTVR	3	0.9997	5
						RQECSPVCGQDQ	2	0.9889	2
						RQECSPVCGQDQ	2	0.9989	7
						RQECSPVCGQDQVT	2	0.9988	5
						RQECSPVCGQDQVTV	2	0.9981	5
						RQECSPVCGQDQVTV	2	0.998	6
						RQECSPVCGQDQVTVAMTPR	3	0.9997	16
						SGIECOLWR	2	0.9997	9
						SPQELLCGASUSDR	2	0.9998	7
						SSTTGPWCYTTPDPTVR	2	0.9989	3
						STTGPWCYTTPDPTVR	2	0.9986	3
						STTHPGADIQENFCR	2	0.9989	5
						TFGSGEADCGLRPLF	2	0.9925	3
						TFGSGEADCGLRPLF	2	0.9865	4
						VTGWNGLK	2	0.9932	2
						WVLTAH	2	0.8499	1
						YGFYTHVFR	2	0.9995	2
						YGFYTHVFR	3	0.9991	1
QS230-1	E9PIF4	E9PIF4_HUMAN	CLNS1A	Methylosome subunit piCln	1.0000	21.23	2	2	3
QS230-2	E9PMI6	E9PMI6_HUMAN	CLNS1A	Methylosome subunit piCln	1.0000	22.75	2	2	3
QS230-3	J3KN38	J3KN38_HUMAN	CLNS1A	Methylosome subunit piCln	1.0000	18.72	2	2	3
QS230-4	P54105	ICLN_HUMAN	CLNS1A	Methylosome subunit piCln	1.0000	16.03	2	2	3
						GLGTGTYIAESR	2	0.9994	1
						LSWLDGSLGSLFYPTISLHALSR	3	0.9524	2
QS231-1	E9PIH4	E9PIH4_HUMAN	RPS3	40S ribosomal protein S3	1.0000	26.96	3	3	8
QS231-2	E9PLO9	E9PLO9_HUMAN	RPS3	40S ribosomal protein S3	1.0000	13.42	3	3	8
QS231-3	E9PPU1	E9PPU1_HUMAN	RPS3	40S ribosomal protein S3	1.0000	19.62	3	3	8
QS231-4	E9PQ96	E9PQ96_HUMAN	RPS3	40S ribosomal protein S3	1.0000	34.07	3	3	8
QS231-5	F22258	F22258_HUMAN	RPS3	40S ribosomal protein S3	1.0000	26.5	3	3	8
QS231-6	P23396	RS3_HUMAN	RPS3	40S ribosomal protein S3	1.0000	12.76	3	3	8
QS231-7	E9PK82	E9PK82_HUMAN	RPS3	40S ribosomal protein S3 (Fragment)	1.0000	24.22	3	3	8
QS231-8	HOYCI7	HOYCI7_HUMAN	RPS3	40S ribosomal protein S3 (Fragment)	1.0000	22.96	3	3	8
QS231-9	HOYEI2	HOYEI2_HUMAN	RPS3	40S ribosomal protein S3 (Fragment)	1.0000	18.13	3	3	8
QS231-10	HOYF32	HOYF32_HUMAN	RPS3	40S ribosomal protein S3 (Fragment)	1.0000	25.2	3	3	8
QS231-11	P23396-2	RS3_HUMAN	RPS3	Isoform 2 of 40S ribosomal protein S3	1.0000	11.97	3	3	8
						AEIENELTR	2	0.9991	2
						ELAEDGYSGVEVR	2	0.9997	5
						TEIILATR	2	0.9984	1

Q5232-1	F8VRJ2	F8VRJ2_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	8.77	1	1	2
Q5232-2	F8VV85	F8VV85_HUMAN	NAP1L1	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	6.21	1	1	2
Q5232-3	E9PJJ2	E9PJJ2_HUMAN	NAP1L4	Nucleosome assembly protein 1-like 4 (Fragment)	1.0000	7.81	1	1	2
Q5232-4	E9PKT8	E9PKT8_HUMAN	NAP1L4	Nucleosome assembly protein 1-like 4 (Fragment)	1.0000	5.92	1	1	2
Q5232-5	E9PNJ7	E9PNJ7_HUMAN	NAP1L4	Nucleosome assembly protein 1-like 4 (Fragment)	1.0000	7.14	1	1	2
Q5232-6	E9PNW0	E9PNW0_HUMAN	NAP1L4	Nucleosome assembly protein 1-like 4 (Fragment)	1.0000	9.35	1	1	2
Q5232-7	E9PS34	E9PS34_HUMAN	NAP1L4	Nucleosome assembly protein 1-like 4 (Fragment)	1.0000	7.52	1	1	2
						FYEYVHDLR	2	0.9994	2
Q5233-1	E9PR48	E9PR48_HUMAN	CRYAB	Alpha-crystallin B chain	1.0000	18.71	3	3	3
Q5233-2	P02511	CRYAB_HUMAN	CRYAB	Alpha-crystallin B chain	1.0000	16.57	3	3	3
Q5233-3	E9PJL7	E9PJL7_HUMAN	CRYAB	Alpha-crystallin B chain (Fragment)	1.0000	22.48	3	3	3
Q5233-4	E9PR44	E9PR44_HUMAN	CRYAB	Alpha-crystallin B chain (Fragment)	1.0000	16.67	3	3	3
						APSWFDTGLSEMR	2	0.9995	1
						FSVNLVDVK	2	0.9658	1
						HFSPEELK	2	0.9879	1
Q5234-1	E9PRY8	E9PRY8_HUMAN	EEF1D	Elongation factor 1-delta	1.0000	11.33	6	7	13
Q5234-2	P29692	EF1D_HUMAN	EEF1D	Elongation factor 1-delta	1.0000	28.11	6	7	13
Q5234-3	E9PK01	E9PK01_HUMAN	EEF1D	Elongation factor 1-delta (Fragment)	1.0000	30.27	6	7	13
Q5234-4	P29692-2	EF1D_HUMAN	EEF1D	isoform 2 of Elongation factor 1-delta	1.0000	12.21	6	7	13
						FYEQMGIPVAGASR	2	0.9997	2
						GVVQELQQAISK	2	0.9996	2
						GVVQELQQAISKLEAR	2	0.9948	1
						GVVQELQQAISKLEAR	3	0.9994	2
						IASLEVENQSLR	2	0.9997	2
						SIQLDGLVWGASK	2	0.9997	2
						SLAGSSGPGASSGTSGDHGELVVR	3	0.9804	2
Q5235-1	G3V1A4	G3V1A4_HUMAN	CFL1	Cofilin 1 (Non-muscle), isoform CRA_a	1.0000	56.38	6	7	14
Q5235-2	E9PK25	E9PK25_HUMAN	CFL1	Cofilin-1	1.0000	41.18	6	7	14
Q5235-3	P23528	COF1_HUMAN	CFL1	Cofilin-1	1.0000	50.6	6	7	14
						AVLFCLSEDKK	2	0.9642	1
						ESKEDLVFIFWAPESAPLK	3	0.9602	2
						KEDLVFIFWAPESAPLK	2	0.9894	1
						KEDLVFIFWAPESAPLK	3	0.9883	2
						LGSASVISLGKPL	2	0.9979	2
						NILEEGKILVGDVGQTDVDPYATFVK	3	0.9989	3
						YALYDATYETK	2	0.9995	3
Q5236-1	P06737	PYGL_HUMAN	PYGL	Glycogen phosphorylase, liver form	0.9994	1.65	1	1	2
Q5236-2	P06737-2	PYGL_HUMAN	PYGL	isoform 2 of Glycogen phosphorylase, liver form	0.9994	1.72	1	1	2
Q5236-3	E9PK47	E9PK47_HUMAN	PYGL	Phosphorylase	0.9994	1.71	1	1	2
						DFNVGDIQAVLDR	2	0.9893	2
Q5237-1	E9PKD5	E9PKD5_HUMAN	PSMC3	26S protease regulatory subunit 6A (Fragment)	1.0000	5.47	2	2	3
						VDIOLDALLR	2	0.999	1
						VIAATNRVOLDPALLR	3	0.9925	2
Q5238-1	P54652	HSP72_HUMAN	HSPA2	Heat shock-related 70 kDa protein 2	1.0000	12.21	6	6	12
Q5238-2	E9PK63	E9PK63_HUMAN	HSPA8	Heat shock cognate 71 kDa protein	1.0000	12.44	6	6	12
Q5238-3	P11142	HSP7C_HUMAN	HSPA8	Heat shock cognate 71 kDa protein	1.0000	12.07	6	6	12
Q5238-4	P11142-2	HSP7C_HUMAN	HSPA8	isoform 2 of Heat shock cognate 71 kDa protein	1.0000	15.92	6	6	12
						ARFEELNADLFR	3	0.9959	2
						IINEPTAAAIAYGLDK	2	0.9947	2
						STAGDTHLGGEDFDNR	2	0.9994	2
						TPPSVAFDTDR	2	0.9997	3
						VEIANDQQGNR	2	0.9988	2
						VQVEYKGETK	2	0.9793	1
Q5239-1	E9PP60	E9PP60_HUMAN	TSTA3	GDP-L-fucose synthase	0.9500	10.43	1	1	2
Q5239-2	Q13630	FCL_HUMAN	TSTA3	GDP-L-fucose synthase	0.9500	3.74	1	1	2
Q5239-3	E9PKL9	E9PKL9_HUMAN	TSTA3	GDP-L-fucose synthase (Fragment)	0.9500	4.48	1	1	2
Q5239-4	E9PLH9	E9PLH9_HUMAN	TSTA3	GDP-L-fucose synthase (Fragment)	0.9500	10.17	1	1	2
Q5239-5	E9PP14	E9PP14_HUMAN	TSTA3	GDP-L-fucose synthase (Fragment)	0.9500	6.06	1	1	2
						ILVTGGSLVGK	2	0.95	2
Q5240-1	E9PKN4	E9PKN4_HUMAN	CSE1	Cold shock domain-containing protein E1 (Fragment)	1.0000	28.26	1	1	2
Q5240-2	E9PLD4	E9PLD4_HUMAN	CSE1	Cold shock domain-containing protein E1 (Fragment)	1.0000	13.83	1	1	2
						LLTSYGFQICSER	2	0.9984	2
Q5241-1	Q14697-2	GANAB_HUMAN	GANAB	isoform 2 of Neutral alpha-glucosidase AB	1.0000	12.94	7	10	18
Q5241-2	E9PKU7	E9PKU7_HUMAN	GANAB	Neutral alpha-glucosidase AB	1.0000	14.67	7	10	18
Q5241-3	FSH6X6	FSH6X6_HUMAN	GANAB	Neutral alpha-glucosidase AB	1.0000	14.76	7	10	18
Q5241-4	Q14697	GANAB_HUMAN	GANAB	Neutral alpha-glucosidase AB	1.0000	13.24	7	10	18
						DLGIFWLNAETWVOISSNTAGK	2	0.9793	1
						FSFGSNTLVSSADPEGHFETPIWIER	3	0.9996	3
						LKVTEGGEPR	2	0.9496	2
						LKVTEGGEPR	3	0.8765	1
						LSFQHDPTSVLVR	2	0.9991	2
						LSFQHDPTSVLVR	3	0.999	2
						LYNLDFQVELYNPMALYGSVPVLLAHNPHR	4	0.9968	1
						RFSGSNTLVSSADPEGHFETPIWIER	3	0.9046	1
						VVIIGAGKPAAVLQTK	2	0.9995	2
						VVIIGAGKPAAVLQTK	3	0.9996	3
Q5242-1	Q5TB19	Q5TB19_HUMAN	ANP32E	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, mem	1.0000	12.75	1	1	2
Q5242-2	E9PLC4	E9PLC4_HUMAN	ANP32E	Acidic leucine-rich nuclear phosphoprotein 32 family membe	1.0000	11.52	1	1	2
						KLEISDNIISGGLEVLAEK	3	0.9965	2
Q5243-1	E9PLJ3	E9PLJ3_HUMAN	CFL1	Cofilin-1 (Fragment)	1.0000	13.92	1	1	3
						YALYDATYETK	2	0.9995	3
Q5244-1	E9PLT0	E9PLT0_HUMAN	CSE1	Cold shock domain-containing protein E1	1.0000	4.04	2	2	3
						ATNIEVLSNTFQFTNEAR	2	0.9994	2
						LLQVYATK	2	0.9753	1
Q5245-1	E9PM54	E9PM54_HUMAN	ILK	Integrin-linked protein kinase	0.9196	4.78	1	1	1
Q5245-2	E9PNR4	E9PNR4_HUMAN	ILK	Integrin-linked protein kinase	0.9196	4.57	1	1	1
Q5245-3	Q13418	ILK_HUMAN	ILK	Integrin-linked protein kinase	0.9196	2.21	1	1	1
Q5245-4	Q13418-2	ILK_HUMAN	ILK	isoform 2 of Integrin-linked protein kinase	0.9196	2.56	1	1	1
						SAVVELIMLR	2	0.9196	1
Q5246-1	E9PM69	E9PM69_HUMAN	PSMC3	26S protease regulatory subunit 6A	1.0000	9.32	3	3	4
Q5246-2	P17980	PR56A_HUMAN	PSMC3	26S protease regulatory subunit 6A	1.0000	8.43	3	3	4
Q5246-3	R4GNH3	R4GNH3_HUMAN	PSMC3	26S protease regulatory subunit 6A	1.0000	8.75	3	3	4
						GATELTHEDYMEGILEVQAK	3	0.9627	1
						VDIOLDALLR	2	0.999	1
						VIAATNRVOLDPALLR	3	0.9925	2
Q5247-1	E9PPT0	E9PPT0_HUMAN	RPS2	40S ribosomal protein S2	0.9856	6.6	1	1	2
Q5247-2	E9PQD7	E9PQD7_HUMAN	RPS2	40S ribosomal protein S2	0.9856	5.53	1	1	2
Q5247-3	P15880	RS2_HUMAN	RPS2	40S ribosomal protein S2	0.9856	4.44	1	1	2
Q5247-4	E9PMM9	E9PMM9_HUMAN	RPS2	40S ribosomal protein S2 (Fragment)	0.9856	5.96	1	1	2
Q5247-5	HOYE27	HOYE27_HUMAN	RPS2	40S ribosomal protein S2 (Fragment)	0.9856	20.63	1	1	2
Q5247-6	HOYEN5	HOYEN5_HUMAN	RPS2	40S ribosomal protein S2 (Fragment)	0.9856	6.67	1	1	2
Q5247-7	H3BNG3	H3BNG3_HUMAN	RPS2	40S ribosomal protein S2 (Fragment)	0.9856	29.55	1	1	2
						SLEEIYFSLPIK	2	0.9856	2
Q5248-1	E9PN89	E9PN89_HUMAN	HSPA8	Heat shock cognate 71 kDa protein (Fragment)	1.0000	5.13	1	1	2
						IINEPTAAAIAYGLDK	2	0.9947	2
Q5249-1	E9PNE6	E9PNE6_HUMAN	HSPA8	Heat shock cognate 71 kDa protein	1.0000	9.4	3	3	7
						ARFEELNADLFR	3	0.9959	2
						GPVAGIDLTYSQVGVFQHGK	3	0.996	2
						TPPSVAFDTDR	2	0.9997	3
Q5250-1	E9PNW4	E9PNW4_HUMAN	CD59	CD59 glycoprotein	1.0000	34.26	4	5	8
Q5250-2	E9PR17	E9PR17_HUMAN	CD59	CD59 glycoprotein	1.0000	28.46	4	5	8
Q5250-3	P13987	CD59_HUMAN	CD59	CD59 glycoprotein	1.0000	28.91	4	5	8
						AGLQVYNK	2	0.9997	1
						CWKFEHCNFDVTR	3	0.9084	1
						FEHCNFDVTR	2	0.9995	2
						FEHCNFDVTR	3	0.9941	1
						LQCYCNPTADCK	2	0.9983	3
Q5251-1	E9PP50	E9PP50_HUMAN	CFL1	Cofilin-1 (Fragment)	1.0000	17.61	2	2	5
Q5251-2	E9PQ87	E9PQ87_HUMAN	CFL1	Cofilin-1 (Fragment)	1.0000	22.95	2	2	5
Q5251-3	Q9Y281	COF2_HUMAN	CFL2	Cofilin-2	1.0000	16.97	2	2	5
Q5251-4	Q9Y281-3	COF2_HUMAN	CFL2	isoform 3 of Cofilin-2	1.0000	18.79	2	2	5
						KEDLVFIFWAPESAPLK	3	0.9983	2
						YALYDATYETK	2	0.9995	3

QS252-1	E9PQH6	E9PQH6_HUMAN	RHOC	Rho-related GTP-binding protein RhoC (Fragment)	1.0000	28.4	5	5	9
						HFCPNVPILVGNKK	3	0.9995	2
						ISAFGYLECSAK	2	0.9886	1
						KLIVVGDGACGK	2	0.9964	1
						LVIVGDGACGK	2	0.984	2
						TCLIVVFSK	2	0.9996	3
QS253-1	E9PRM1	E9PRM1_HUMAN	CAPN1	Calpain-1 catalytic subunit	1.0000	14.43	2	2	4
						LVFVHSAFGNFWVSALLEK	3	0.9978	3
						YLGDQYEQRLR	2	0.9992	1
QS254-1	Q9NPQ8-3	RIC8A_HUMAN	RIC8A	Isoform 3 of Synembryon-A	1.0000	6.89	2	3	7
QS254-2	Q9NPQ8-4	RIC8A_HUMAN	RIC8A	Isoform 4 of Synembryon-A	1.0000	6.98	2	3	7
QS254-3	Q9NPQ8	RIC8A_HUMAN	RIC8A	Synembryon-A	1.0000	6.97	2	3	7
QS254-4	E9PSI0	E9PSI0_HUMAN	RIC8A	Synembryon-A (Fragment)	1.0000	20.22	2	3	7
						AVAEAVETGEEDVIMEALR	2	0.9997	3
						AVAEAVETGEEDVIMEALR	3	0.9397	1
						LAELLVSVLEQGLPPSHR	3	0.9982	3
QS255-1	Q72406-2	MYH14_HUMAN	MYH14	Isoform 2 of Myosin-14	1.0000	16.31	26	31	51
QS255-2	Q72406-6	MYH14_HUMAN	MYH14	Isoform 6 of Myosin-14	1.0000	16.58	26	31	51
QS255-3	F222U8	F222U8_HUMAN	MYH14	Myosin-14	1.0000	16.37	26	31	51
QS255-4	G8LI9	G8LI9_HUMAN	MYH14	Myosin-14	1.0000	16.31	26	31	51
QS255-5	Q72406	MYH14_HUMAN	MYH14	Myosin-14	1.0000	16.64	26	31	51
						AEAECAEAETR	2	0.9995	2
						AEISSLQAT	2	0.9766	1
						AMEAEAGLRQLEEEAAR	3	0.936	1
						AQAELENVSGALNEASK	2	0.9997	3
						AQVTEDELTAADAK	2	0.9997	3
						DLGEELEALRGLEDLTDSNAQQLR	3	0.9986	3
						EAQAALAEAQEDLESE	2	0.9997	1
						ELFQETLESLR	2	0.9705	1
						ELQTAAQQLSEWR	2	0.9996	3
						ELLSTEAQLHDAQQLQGETR	3	0.9977	2
						FDQLLAEEK	2	0.9825	1
						HGOALGELAEQLQEAR	3	0.9993	3
						IHEAAVQELR	2	0.9994	1
						IHEAAVQELR	3	0.9921	1
						ILFQEFF	2	0.9921	1
						KEEELQAALAR	2	0.9991	2
						KEEELQAALAR	3	0.996	1
						KFDQLLAEEK	2	0.9778	1
						KQELLEVSELEAR	2	0.9993	2
						KQELLEVSELEAR	3	0.9995	2
						LAEFFSQAAEEEEK	2	0.9634	1
						LAEFFSQAAEEEEKVK	2	0.9974	1
						LALAEVSELR	2	0.9997	1
						LALAEVSELRAEISSLQAT	3	0.9994	3
						LAQAEQLQGETR	2	0.9996	2
						LQHQIQEIAHLEAEGAR	3	0.998	1
						RLEQLQLEVGQR	2	0.9963	1
						RLEQLQLEVGQR	3	0.9888	2
						RQEEFAGALEAGEAR	2	0.9992	1
						RQEEFAGALEAGEAR	3	0.9185	1
						VAEQAANDLR	2	0.9997	2
QS256-1	F22ZY4	F22ZY4_HUMAN	PDXK	Pyridoxal kinase	1.0000	12.13	2	2	3
QS256-2	O00764	PDXK_HUMAN	PDXK	Pyridoxal kinase	1.0000	10.58	2	2	3
						DKSFLAMVVDIVQELK	3	0.979	2
						GQVLSDELQELYEGLR	2	0.9993	1
QS257-1	Q14914-2	PTGR1_HUMAN	PTGR1	Isoform 2 of Prostaglandin reductase 1	0.9947	6.64	2	2	2
QS257-2	Q5IWP3	Q5IWP3_HUMAN	PTGR1	Leukotriene B4 12-hydroxylase, isoform CRA_d	0.9947	11.3	2	2	2
QS257-3	Q14914	PTGR1_HUMAN	PTGR1	Prostaglandin reductase 1	0.9947	6.08	2	2	2
QS257-4	F22J19	F22J19_HUMAN	PTGR1	Prostaglandin reductase 1 (Fragment)	0.9947	16.95	2	2	2
						IAICGAISTYNR	2	0.9518	1
						MEAFVVR	2	0.8996	1
QS258-1	F22K5	F22K5_HUMAN	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	1.0000	7.41	1	1	3
QS258-2	Q5IYR4	Q5IYR4_HUMAN	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	1.0000	7.23	1	1	3
QS258-3	Q5IYR7	Q5IYR7_HUMAN	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	1.0000	3.49	1	1	3
						SIVEIEDLVAR	2	0.9997	3
QS259-1	F5GW6	F5GW6_HUMAN	CCT2	T-complex protein 1 subunit beta	1.0000	5.09	2	2	6
QS259-2	F8VQ14	F8VQ14_HUMAN	CCT2	T-complex protein 1 subunit beta	1.0000	6.49	2	2	6
						GATQQLIDEAR	2	0.9992	3
						LTSFGIAIAGDLVK	2	0.9997	3
QS260-1	F5GWY2	F5GWY2_HUMAN	ATIC	Phosphoribosylaminoimidazolecarboxamide formyltransferase	1.0000	15.76	6	7	22
						DLNATIAVK	2	0.9994	2
						EVSDGIIAPGYEEAALTISK	2	0.9994	6
						EVSDGIIAPGYEEAALTISK	3	0.9968	2
						LDNFLIR	2	0.9996	2
						TLFGHLISQK	2	0.9671	1
						TVASPGVTVEAEQIDIGVTLR	3	0.9996	6
						VVACNLVPVK	2	0.9995	3
QS261-1	F5GX14	F5GX14_HUMAN	MLEC	Malectin	0.9999	16.13	2	2	4
QS261-2	Q14165	MLEC_HUMAN	MLEC	Malectin	0.9999	11.99	2	2	4
QS261-3	F5H1S8	F5H1S8_HUMAN	MLEC	Malectin (Fragment)	0.9999	23.97	2	2	4
						FAEYVFAQSQK	2	0.9992	3
						YNEETFGYEPKPEGDGVVLVK	3	0.8515	1
QS262-1	F5H5J4	F5H5J4_HUMAN	LDHA	L-lactate dehydrogenase A chain	1.0000	16.85	1	1	3
QS262-2	F5H6W8	F5H6W8_HUMAN	LDHA	L-lactate dehydrogenase A chain	1.0000	15.96	1	1	3
QS262-3	F5GXH2	F5GXH2_HUMAN	LDHA	L-lactate dehydrogenase A chain (Fragment)	1.0000	13.16	1	1	3
QS262-4	F5GXV2	F5GXV2_HUMAN	LDHA	L-lactate dehydrogenase A chain (Fragment)	1.0000	9.62	1	1	3
QS262-5	F5GYU2	F5GYU2_HUMAN	LDHA	L-lactate dehydrogenase A chain (Fragment)	1.0000	10.42	1	1	3
QS262-6	F5G2Q4	F5G2Q4_HUMAN	LDHA	L-lactate dehydrogenase A chain (Fragment)	1.0000	20.83	1	1	3
						DLADELALVDVIEDK	2	0.9992	3
QS263-1	F5GXR3	F5GXR3_HUMAN	PTMS	Parathyrimosin	0.9544	10.58	1	1	1
QS263-2	P20962	PTMS_HUMAN	PTMS	Parathyrimosin	0.9544	10.78	1	1	1
QS263-3	F5H7R9	F5H7R9_HUMAN	PTMS	Parathyrimosin (Fragment)	0.9544	19.3	1	1	1
						SVEAAEELSAK	2	0.9544	1
QS264-1	F5GXS2	F5GXS2_HUMAN	ACTN4	Alpha-actinin-4	1.0000	7.68	3	3	7
QS264-2	H7C144	H7C144_HUMAN	ACTN4	Alpha-actinin-4 (Fragment)	1.0000	11.7	3	3	7
QS264-3	Q43707-3	ACTN4_HUMAN	ACTN4	Isoform 3 of Alpha-actinin-4	1.0000	7.68	3	3	7
						ETDSDTDADQVIASF	2	0.9991	2
						TINEVENQLTR	2	0.999	2
						VGWEQLLTIAR	2	0.9996	3
QS265-1	F5GV79	F5GV79_HUMAN	PTPN6	Tyrosine-protein phosphatase non-receptor type 6 (Fragment)	0.9999	6.25	1	1	1
QS265-2	F5H0N8	F5H0N8_HUMAN	PTPN6	Tyrosine-protein phosphatase non-receptor type 6 (Fragment)	0.9999	5.45	1	1	1
QS265-3	F5H1Z8	F5H1Z8_HUMAN	PTPN6	Tyrosine-protein phosphatase non-receptor type 6 (Fragment)	0.9999	6	1	1	1
QS265-4	F5H5H9	F5H5H9_HUMAN	PTPN6	Tyrosine-protein phosphatase non-receptor type 6 (Fragment)	0.9999	6.92	1	1	1
						VGQDVTHIR	2	0.9916	1
QS266-1	F5GY80	F5GY80_HUMAN	C8B	Complement component C8 beta chain	1.0000	22.68	12	14	32
QS266-2	F5H7G1	F5H7G1_HUMAN	C8B	Complement component C8 beta chain	1.0000	22.26	12	14	32
QS266-3	P07358	C08B_HUMAN	C8B	Complement component C8 beta chain	1.0000	20.3	12	14	32
						DTMVEDLVVLR	2	0.9995	3
						ELVTATDFAYSSTVR	2	0.995	3
						GDYTLNNVHACAK	2	0.9997	3
						GGASEHITLAVQELPTADLMQEWGDVQYNPAIK	3	0.9906	1
						GILNEIKDR	2	0.943	1
						LPLEYSYGEYR	2	0.9994	5
						RPLEYSYGEYR	2	0.979	1
						SDLEVAHYK	2	0.9943	2
						SVFLHAR	2	0.9625	1
						TATDFAYSSTVR	2	0.8146	1
						VENPLVELVATDFAYSSTVR	2	0.9997	2
						VKPELVYELVATDFAYSSTVR	3	0.994	2
						VKPELVYELVATDFAYSSTVR	2	0.9985	1
						VKPELVYELVATDFAYSSTVR	3	0.9987	6
QS267-1	F5GYI5	F5GYI5_HUMAN	KRT85	Keratin, type II cuticular Hb5	1.0000	7.8	2	2	4

QS267-2	P78386	KRT85_HUMAN	KRT85	Keratin, type II cuticular Hb5	1.0000	4.54	2	2	4
						DLNMDCIAEIK	2	0.9989	2
						LGLDIEIATYR	2	0.9976	2
QS268-1	F5GYJ8	F5GYJ8_HUMAN	OTUB1	Ubiquitin thioesterase OTUB1	1.0000	25.52	7	7	9
QS268-2	F5GYN4	F5GYN4_HUMAN	OTUB1	Ubiquitin thioesterase OTUB1	1.0000	30.29	7	7	9
QS268-3	J3KR44	J3KR44_HUMAN	OTUB1	Ubiquitin thioesterase OTUB1	1.0000	23.7	7	7	9
QS268-4	Q96FW1	OTUB1_HUMAN	OTUB1	Ubiquitin thioesterase OTUB1	1.0000	26.94	7	7	9
						AFGFSHLEALDDSK	3	0.9681	1
						AFGFSHLEALDDSKELQR	3	0.9746	2
						EYAEDDNIYQOK	2	0.9989	1
						FFEHFIEGGR	3	0.9858	2
						IQQEIADVQNPVLSER	2	0.9997	1
						LELSVLYK	2	0.9969	1
						LLTSGLVLR	2	0.9615	1
QS269-1	F5GYR8	F5GYR8_HUMAN	USO1	General vesicular transport factor p115	1.0000	2.78	2	2	4
QS269-2	F5H4X1	F5H4X1_HUMAN	USO1	General vesicular transport factor p115	1.0000	2.85	2	2	4
QS269-3	O60763	USO1_HUMAN	USO1	General vesicular transport factor p115	1.0000	2.81	2	2	4
QS269-4	H0Y7C0	H0Y7C0_HUMAN	USO1	General vesicular transport factor p115 (Fragment)	1.0000	4.23	2	2	4
QS269-5	O60763-2	USO1_HUMAN	USO1	isoform 2 of General vesicular transport factor p115	1.0000	2.77	2	2	4
						SQNSQSVEITK	2	0.9995	2
						SVEVQGETETIATK	2	0.9997	2
QS270-1	M0R1V7	M0R1V7_HUMAN	UBA52	Ubiquitin-60S ribosomal protein L40 (Fragment)	1.0000	25.4	1	1	3
QS270-2	J3QSA3	J3QSA3_HUMAN	UBB	Ubiquitin (Fragment)	1.0000	37.21	1	1	3
QS270-3	F5GZ39	F5GZ39_HUMAN	UBC	Polyubiquitin-C (Fragment)	1.0000	26.23	1	1	3
						TITLEVEPSDTIENVK	2	0.9996	3
QS271-1	Q9Y493-2	ZAN_HUMAN	ZAN	Isoform 1 of Zonadhesin	0.9719	0.33	1	1	1
QS271-2	Q9Y493-3	ZAN_HUMAN	ZAN	Isoform 2 of Zonadhesin	0.9719	0.33	1	1	1
QS271-3	Q9Y493-4	ZAN_HUMAN	ZAN	Isoform 4 of Zonadhesin	0.9719	0.34	1	1	1
QS271-4	Q9Y493-5	ZAN_HUMAN	ZAN	Isoform 5 of Zonadhesin	0.9719	0.35	1	1	1
QS271-5	Q9Y493-6	ZAN_HUMAN	ZAN	Isoform 6 of Zonadhesin	0.9719	0.33	1	1	1
QS271-6	Q9Y493-7	ZAN_HUMAN	ZAN	Isoform 7 of Zonadhesin	0.9719	0.31	1	1	1
QS271-7	F5GZ55	F5GZ55_HUMAN	ZAN	Zonadhesin	0.9719	0.33	1	1	1
QS271-8	F5H0T8	F5H0T8_HUMAN	ZAN	Zonadhesin	0.9719	0.33	1	1	1
QS271-9	F5H4B5	F5H4B5_HUMAN	ZAN	Zonadhesin	0.9719	0.34	1	1	1
QS271-10	Q9Y493	ZAN_HUMAN	ZAN	Zonadhesin	0.9719	0.32	1	1	1
						GVFLGASGR	2	0.9719	1
QS272-1	P63096-2	GNAI1_HUMAN	GNAI1	Isoform 2 of Guanine nucleotide-binding protein G(i) subunit	1.0000	9.27	2	2	3
QS272-2	F5GZL8	F5GZL8_HUMAN	GNAI2	Guanine nucleotide-binding protein G(i) subunit alpha-2	1.0000	10.22	2	2	3
						EYTHFTCATDITK	2	0.9958	2
						NVQVFVDVTDVIK	2	0.9937	1
QS273-1	F5GZQ3	F5GZQ3_HUMAN	HADHB	3-ketoacyl-CoA thiolase	0.9998	5.45	2	2	2
QS273-2	P55084-2	ECHB_HUMAN	HADHB	Isoform 2 of Trifunctional enzyme subunit beta, mitochondrial	0.9998	5.53	2	2	2
QS273-3	P55084	ECHB_HUMAN	HADHB	Trifunctional enzyme subunit beta, mitochondrial	0.9998	5.27	2	2	2
						EVVDVIRGTVIQEVK	2	0.9932	1
						LEQDEIARL	2	0.9675	1
QS274-1	F5H1V0	F5H1V0_HUMAN	C1R	Complement C1r subcomponent	1.0000	13.89	1	1	3
QS274-2	F5GZR1	F5GZR1_HUMAN	C1R	Complement C1r subcomponent (Fragment)	1.0000	5.56	1	1	3
QS274-3	F5H2D0	F5H2D0_HUMAN	C1R	Complement C1r subcomponent (Fragment)	1.0000	6.41	1	1	3
QS274-4	F5H3N3	F5H3N3_HUMAN	C1R	Complement C1r subcomponent (Fragment)	1.0000	12.82	1	1	3
QS274-5	F5H6Y3	F5H6Y3_HUMAN	C1R	Complement C1r subcomponent (Fragment)	1.0000	12.82	1	1	3
QS274-6	F6T9X8	F6T9X8_HUMAN	C1R	Complement C1r subcomponent (Fragment)	1.0000	5.78	1	1	3
						LVFQQDFLEPSEGCFYDVYK	2	0.9993	3
QS275-1	P52597	HNRPF_HUMAN	HNRNPF	Heterogeneous nuclear ribonucleoprotein F	1.0000	2.41	1	1	2
QS275-2	F5GZT4	F5GZT4_HUMAN	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H	1.0000	6.29	1	1	2
QS275-3	H0YB07	H0YB07_HUMAN	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H (Fragment)	1.0000	5.15	1	1	2
QS275-4	H0YB67	H0YB67_HUMAN	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H (Fragment)	1.0000	5.41	1	1	2
						VHIGSGRGR	2	0.9986	2
QS276-1	F5H0C7	F5H0C7_HUMAN	ARF3	ADP-ribosylation factor 3 (Fragment)	1.0000	34.11	2	2	4
						LGEIVTTIPTIGFNVETVEYK	2	0.9984	2
						NISFTVWDVGGQDK	2	0.9894	2
QS277-1	Q86UK7	URP2_HUMAN	FERMT3	Fermitin family homolog 3	0.9985	2.4	1	1	2
QS277-2	F5H1C6	F5H1C6_HUMAN	FERMT3	Fermitin family homolog 3 (Fragment)	0.9985	5.59	1	1	2
QS277-3	Q86UK7-2	URP2_HUMAN	FERMT3	Isoform 2 of Fermitin family homolog 3	0.9985	2.41	1	1	2
						VFVGGEDEPEASVTLR	2	0.9978	2
QS278-1	F5H283	F5H283_HUMAN	SPOCK2	Testican-2	1.0000	12.97	5	5	9
QS278-2	Q92563	TICN2_HUMAN	SPOCK2	Testican-2	1.0000	12.97	5	5	9
						DSIGWMFSK	2	0.9982	2
						IQIQEAAK	2	0.9826	1
						LEQQAQLSSK	2	0.9997	3
						SWEDNQSGEALDITK	3	0.9214	1
						VSTAECWCFWR	2	0.9997	2
QS279-1	F5H2F4	F5H2F4_HUMAN	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic	1.0000	2.25	2	2	2
QS279-2	P11586	CLTC_HUMAN	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic	1.0000	2.46	2	2	2
QS279-3	V9GY3	V9GY3_HUMAN	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic (Fragment)	1.0000	21.5	2	2	2
						GVPTGFLPIR	2	0.9748	1
						THLSLSHNPEQK	2	0.9897	1
QS280-1	P52566	GDIR2_HUMAN	ARHGDIIB	Rho GDP-dissociation inhibitor 2	0.9599	3.98	1	1	2
QS280-2	F5H2R5	F5H2R5_HUMAN	ARHGDIIB	Rho GDP-dissociation inhibitor 2 (Fragment)	0.9599	9.09	1	1	2
QS280-3	F5H3P3	F5H3P3_HUMAN	ARHGDIIB	Rho GDP-dissociation inhibitor 2 (Fragment)	0.9599	5.06	1	1	2
QS280-4	F5H6Q0	F5H6Q0_HUMAN	ARHGDIIB	Rho GDP-dissociation inhibitor 2 (Fragment)	0.9599	7.14	1	1	2
QS280-5	H0Y6X7	H0Y6X7_HUMAN	ARHGDIIB	Rho GDP-dissociation inhibitor 2 (Fragment)	0.9599	4.1	1	1	2
						APNVVYTR	2	0.9599	2
QS281-1	F5H335	F5H335_HUMAN	EIF3A	Eukaryotic translation initiation factor 3 subunit A	1.0000	4.9	5	5	10
QS281-2	Q14152	EIF3A_HUMAN	EIF3A	Eukaryotic translation initiation factor 3 subunit A	1.0000	4.78	5	5	10
						FNVLQYVPEVK	2	0.9996	3
						LTSLVPFVDQFLER	2	0.9979	2
						NQLTAMSSVLAK	2	0.9976	2
						TLSGSDLNAYTR	2	0.9995	2
						VLLATLSIPITPER	2	0.9902	1
QS282-1	F5H3T8	F5H3T8_HUMAN	RARS	Arginine-tRNA ligase, cytoplasmic	1.0000	4.63	2	2	5
QS282-2	P54136-2	SYRC_HUMAN	RARS	Isoform Monomeric of Arginine-tRNA ligase, cytoplasmic	1.0000	3.57	2	2	5
						LFEFAGYDVLRL	2	0.9996	3
						STIGESISR	2	0.9856	2
QS283-1	F5H423	F5H423_HUMAN		Uncharacterized protein	1.0000	26.67	4	4	7
QS283-2	P84077	ARF1_HUMAN	ARF1	ADP-ribosylation factor 1	1.0000	30.94	4	4	7
QS283-3	P61204	ARF3_HUMAN	ARF3	ADP-ribosylation factor 3	1.0000	30.94	4	4	7
						DAVLIVFANK	2	0.9531	1
						ILMVGLDAAGK	2	0.9979	2
						LGEIVTTIPTIGFNVETVEYK	2	0.9984	2
						NISFTVWDVGGQDK	2	0.9894	2
QS284-1	F5H4D6	F5H4D6_HUMAN	G3BP1	Ras GTPase-activating protein-binding protein 1	0.9064	4.58	1	1	1
QS284-2	Q13283	G3BP1_HUMAN	G3BP1	Ras GTPase-activating protein-binding protein 1	0.9064	2.79	1	1	1
						DFQSYGNVVELR	2	0.9064	1
QS285-1	F5H4R9	F5H4R9_HUMAN	DNM2	Dynamitin-2	1.0000	14.14	9	9	13
QS285-2	P50570	DYN2_HUMAN	DNM2	Dynamitin-2	1.0000	14.14	9	9	13
QS285-3	P50570-2	DYN2_HUMAN	DNM2	Isoform 2 of Dynamitin-2	1.0000	14.2	9	9	13
QS285-4	P50570-3	DYN2_HUMAN	DNM2	Isoform 3 of Dynamitin-2	1.0000	14.14	9	9	13
QS285-5	P50570-4	DYN2_HUMAN	DNM2	Isoform 4 of Dynamitin-2	1.0000	14.14	9	9	13
QS285-6	P50570-5	DYN2_HUMAN	DNM2	Isoform 5 of Dynamitin-2	1.0000	14.15	9	9	13
						DMILQFISR	2	0.9996	2
						EVDPGQLR	2	0.9416	1
						GISPVPINLR	2	0.9985	2
						HVFIAFNTQGR	2	0.9825	1
						LQDAFSSIGQSLDLPQIAVVGGSAGK	3	0.9909	2
						NLVDYSVAIINK	2	0.9991	2
						SSLVNFVGR	2	0.9953	1
						VYPGDDPPDIEYQIK	2	0.9996	1
						VYSPHVLNLTLDLPGITK	3	0.9971	1
QS286-1	F5H5D3	F5H5D3_HUMAN	TUBA1C	Tubulin alpha-1C chain	1.0000	32.76	13	15	36
QS286-2	Q9BGE3	TBA1C_HUMAN	TUBA1C	Tubulin alpha-1C chain	1.0000	37.86	13	15	36
						AVCMLSNTTAAEAWAR	2	0.9997	3
						AVFDLEPTVIDEVR	2	0.9997	4
						AVFDLEPTVIDEVR	3	0.9996	2

						AYHQLTVAEITNACFEPAQMVK	3	0.992	2
						DVNAIAITK	2	0.999	2
						ECISIHVGQAGVQIGNACWEL	2	0.9109	1
						ECISIHVGQAGVQIGNACWELY	2	0.9069	1
						EIDLVLDLDR	2	0.9997	4
						GHTYTGKEIDLVLDLDR	3	0.9994	2
						KLADQCTGLDGF	2	0.9089	1
						LADQCTGLDGLVYHSGGGTSGFTSLLMER	3	0.9909	1
						TIGGGDGSFNTFFSETGAGK	2	0.9997	8
						TIGGGDGSFNTFFSETGAGK	3	0.9851	1
						TIQFVDWCPTGFK	2	0.9995	3
						VOLEPTVIDEVR	2	0.8948	1
QS287-1	F5H5Y3	F5H5Y3_HUMAN	SRP68	Signal recognition particle subunit SRP68	1.0000	6.27	2	2	3
						FETFCLDPSLVTK	2	0.9983	2
						SGGTGLLAELKLEALITQTR	3	0.9664	1
QS288-1	O00159-2	MYO1C_HUMAN	MYO1C	Isoform 2 of Unconventional myosin-1c	1.0000	2.63	2	2	3
QS288-2	O00159-3	MYO1C_HUMAN	MYO1C	Isoform 3 of Unconventional myosin-1c	1.0000	2.59	2	2	3
QS288-3	F5H6E2	F5H6E2_HUMAN	MYO1C	Unconventional myosin-1c	1.0000	2.6	2	2	3
QS288-4	O00159	MYO1C_HUMAN	MYO1C	Unconventional myosin-1c	1.0000	2.54	2	2	3
						LLOFYAETCPAPER	2	0.9986	2
						MSLLQLVEILQSK	2	0.9997	1
QS289-1	P61769	B2MG_HUMAN	B2M	Beta-2-microglobulin	1.0000	48.74	5	6	11
QS289-2	F5H6I0	F5H6I0_HUMAN	B2M	Beta-2-microglobulin form pl 5.3	1.0000	47.54	5	6	11
						DWSFYLLVYTFPTTEKDEYACR	3	0.8132	1
						IEKVEHSDLSFSK	2	0.9993	3
						SNFLNCYVSGFHPSDIEV	2	0.9079	1
						SNFLNCYVSGFHPSDIEVDLLK	2	0.9376	1
						SNFLNCYVSGFHPSDIEVDLLK	3	0.9996	4
						VEHSDLSFSK	3	0.9338	1
QS290-1	F5H6T1	F5H6T1_HUMAN	ACTR2	Actin-related protein 2	1.0000	8.85	2	2	2
QS290-2	P61160-2	ARP2_HUMAN	ACTR2	Isoform 2 of Actin-related protein 2	1.0000	6.77	2	2	2
						GYAFNHSADFETVR	2	0.999	1
						LCVGVNIEQEQQ	2	0.9829	1
QS291-1	P19827	ITIH1_HUMAN	ITIH1	Inter-alpha-trypsin inhibitor heavy chain H1	1.0000	23.27	21	23	54
QS291-2	F5H7E1	F5H7E1_HUMAN	ITIH1	Uncharacterized protein	1.0000	32.87	21	23	54
						AAISGENAGLVR	2	0.9991	2
						ADVQAHGGEQFSITCLVDEEMK	3	0.9815	2
						AHYVVTSQVVTANEAR	3	0.905	1
						DYFDLVLFGR	2	0.9563	2
						EVAFDLEPK	2	0.9996	3
						FAHYVVTSQVVTANEAR	2	0.9997	3
						GFLSDEATNLGGLLR	2	0.9995	4
						GSLSVQASEANLQAQDFVR	2	0.9997	3
						GSLSVQASEANLQAQDFVR	3	0.9923	2
						KAISISENAGLVR	2	0.9724	1
						LDAQASFLPK	2	0.9951	5
						LWAYLTQIELLAK	2	0.9997	5
						LWAYLTQIELLAK	3	0.9963	2
						LWAYLTQIELLAKR	3	0.9194	1
						MSLDYGFVTPLTSMISR	2	0.9337	2
						QAVDTADVGVFIR	2	0.9989	4
						QYEGSEIVVAGR	2	0.9997	2
						TAFISDFAVTADGNAFIGDIK	2	0.9994	2
						VTQLTYEEVLK	2	0.9995	2
						VTFLTYEEVLKR	2	0.8553	1
						VTSQVVTANEAR	2	0.9807	1
						VVTSQVVTANEAR	2	0.9844	2
						YFDLVLFGR	2	0.983	2
QS292-1	F5H7T4	F5H7T4_HUMAN	C15	Complement C15 subcomponent (Fragment)	1.0000	17.83	2	2	4
						GFGQVVTLR	2	0.9993	3
						QFGPYCGHGFPGPLNIETK	3	0.9533	1
QS293-1	P08709	FA7_HUMAN	F7	Coagulation factor VII	1.0000	11.8	4	5	12
QS293-2	F5H8B0	F5H8B0_HUMAN	F7	Factor VII heavy chain	1.0000	13.85	4	5	12
QS293-3	P08709-2	FA7_HUMAN	F7	Isoform B of Coagulation factor VII	1.0000	12.39	4	5	12
						DQLQSYICFLPAFEGR	2	0.9997	5
						DQLQSYICFLPAFEGR	3	0.9714	2
						FSLVSGWGQLLDR	2	0.9996	2
						GATALEMLVNLNVR	2	0.9943	2
						LMTQDCQGSQR	2	0.9438	1
QS294-1	H78294	H78294_HUMAN	P4HB	Protein disulfide-isomerase	1.0000	13.15	5	6	10
QS294-2	F5H8J2	F5H8J2_HUMAN	P4HB	Uncharacterized protein	1.0000	13.53	5	6	10
						DAPEEEDHVLVLR	2	0.9576	2
						NFEDVAFDEKK	2	0.9838	1
						THILLFLPK	2	0.9987	2
						VDATEESDLAQQYGVNR	2	0.9997	2
						YKPESEELTAER	2	0.9994	1
						YKPESEELTAER	3	0.9985	2
QS295-1	F6RFDS	F6RFDS_HUMAN	DSTN	Dextrin	1.0000	40.74	4	4	10
QS295-2	P60981	DEST_HUMAN	DSTN	Dextrin	1.0000	33.33	4	4	10
QS295-3	P60981-2	DEST_HUMAN	DSTN	Isoform 2 of Dextrin	1.0000	37.16	4	4	10
						AVIFCLSDAKK	2	0.9463	1
						ELVGDGVGVTTDPPK	2	0.9989	1
						KEELMFLWAPLAPLKL	3	0.9993	5
						VALYDASFETK	2	0.9993	3
QS296-1	F6U211	F6U211_HUMAN	RPS10	40S ribosomal protein S10	0.9771	5.23	1	1	2
QS296-2	P46783	RS10_HUMAN	RPS10	40S ribosomal protein S10	0.9771	5.45	1	1	2
QS296-3	S4R435	S4R435_HUMAN	RPS10-NUDT3	Protein RPS10-NUDT3 (Fragment)	0.9771	3.15	1	1	2
						IAIYELLFK	2	0.9771	2
QS297-1	F6UT28	F6UT28_HUMAN	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta	1.0000	7.88	1	1	1
QS297-2	F6X3N5	F6X3N5_HUMAN	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta	1.0000	7.98	1	1	1
						ELAGHTGYLSCCR	2	0.9973	1
QS298-1	P50502	F10A1_HUMAN	ST13	Hsc70-interacting protein	1.0000	10.03	3	3	7
QS298-2	F6VDH7	F6VDH7_HUMAN	ST13	Hsc70-interacting protein (Fragment)	1.0000	22.84	3	3	7
QS298-3	H7C3I1	H7C3I1_HUMAN	ST13	Hsc70-interacting protein (Fragment)	1.0000	25.34	3	3	7
QS298-4	Q8I2P2	ST134_HUMAN	ST13P4	Putative protein FAM10A4	1.0000	15.42	3	3	7
						AIDLFTDAIK	2	0.9861	2
						AIENPDSAQPYK	2	0.9995	3
						VAAIEALNDGELQK	2	0.9996	2
QS299-1	F8VW50	F8VW50_HUMAN	RPLP0	60S acidic ribosomal protein P0	1.0000	4.27	1	1	3
QS299-2	G3V210	G3V210_HUMAN	RPLP0	60S acidic ribosomal protein P0	1.0000	7.23	1	1	3
QS299-3	Q3B7A4	Q3B7A4_HUMAN	RPLP0	60S acidic ribosomal protein P0	1.0000	4.71	1	1	3
QS299-4	F8VPF8	F8VPF8_HUMAN	RPLP0	60S acidic ribosomal protein P0 (Fragment)	1.0000	7.84	1	1	3
QS299-5	F8VU65	F8VU65_HUMAN	RPLP0	60S acidic ribosomal protein P0 (Fragment)	1.0000	4.86	1	1	3
QS299-6	F8VW21	F8VW21_HUMAN	RPLP0	60S acidic ribosomal protein P0 (Fragment)	1.0000	4.92	1	1	3
QS299-7	Q8NHW5	RLA0L_HUMAN	RPLP0P6	60S acidic ribosomal protein P0-like	1.0000	3.79	1	1	3
						TSFFQALGITTK	2	0.9997	3
QS300-1	F8VPF3	F8VPF3_HUMAN	MYL6	Myosin light polypeptide 6 (Fragment)	1.0000	20	2	2	4
						ALQGNPPTNAEVLK	2	0.9994	2
						DQGTGYEDYVEGLR	2	0.9909	2
QS301-1	Q9UH86-4	LIMA1_HUMAN	LIMA1	Isoform 4 of LIM domain and actin-binding protein 1	0.9996	2.76	2	2	2
QS301-2	F8VRN8	F8VRN8_HUMAN	LIMA1	LIM domain and actin-binding protein 1	0.9996	5.41	2	2	2
QS301-3	Q9UH86	LIMA1_HUMAN	LIMA1	LIM domain and actin-binding protein 1	0.9996	2.77	2	2	2
QS301-4	F8VTU2	F8VTU2_HUMAN	LIMA1	LIM domain and actin-binding protein 1 (Fragment)	0.9996	16.15	2	2	2
QS301-5	F8VVQ7	F8VVQ7_HUMAN	LIMA1	LIM domain and actin-binding protein 1 (Fragment)	0.9996	18.92	2	2	2
						SENTENLSQHFR	2	0.9903	1
						SSAIVEIFSK	2	0.9817	1
QS302-1	F8VTQ5	F8VTQ5_HUMAN	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	1.0000	26.21	4	4	11
						IEVIEIMTDR	2	0.9984	2
						KLFIGGLSFETTDLSLR	2	0.9997	2
						LFIGGLSFETTDLSLR	2	0.9997	3
						SESPKEPEQLR	2	0.9968	4
QS303-1	G3V203	G3V203_HUMAN	RPL18	60S ribosomal protein L18	1.0000	7.93	1	1	2
QS303-2	Q07020	RL18_HUMAN	RPL18	60S ribosomal protein L18	1.0000	6.91	1	1	2

Q5303-3	F8VUA6	F8VUA6_HUMAN	RPL18	60S ribosomal protein L18 (Fragment)	1.0000	10	1	1	2
Q5303-4	HOYHA7	HOYHA7_HUMAN	RPL18	60S ribosomal protein L18 (Fragment)	1.0000	7.78	1	1	2
Q5303-5	J3QQ67	J3QQ67_HUMAN	RPL18	60S ribosomal protein L18 (Fragment)	1.0000	6.84	1	1	2
Q5303-6	Q07020-2	RL18_HUMAN	RPL18	isoform 2 of 60S ribosomal protein L18	1.0000	8.18	1	1	2
							ILTFDQLALDSPK	2	0.9992
Q5304-1	F8VV32	F8VV32_HUMAN	LYZ	Lysozyme C	1.0000	29.81	3	2	6
							GISLANWMCIAK	2	0.9884
							LGMDSGYR	2	0.9993
							STDYGFQINSR	2	0.9996
Q5305-1	F8VZ49	F8VZ49_HUMAN	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	1.0000	6.93	1	1	3
Q5305-2	Q32P51	RA112_HUMAN	HNRNPA1L2	Heterogeneous nuclear ribonucleoprotein A1-like 2	1.0000	5	1	1	3
							LFIGGLSFETDESIR	2	0.9997
Q5306-1	F8VZ9Y	F8VZ9Y_HUMAN	KRT18	Keratin, type I cytoskeletal 18	1.0000	48.08	18	21	29
Q5306-2	P05783	K1C18_HUMAN	KRT18	Keratin, type I cytoskeletal 18	1.0000	43.72	18	21	29
							AQIFANTVDNAR	2	0.9996
							AQYDELARK	2	0.9957
							ASLENSLR	2	0.818
							DWSHYFK	2	0.998
							GLQAQIASGSLTVEVDAPK	2	0.9997
							GLQAQIASGSLTVEVDAPK	3	0.9987
							IVLQIDNAR	2	0.9996
							KVIDDTNTR	2	0.9983
							LEAEIATYR	2	0.9935
							LQLETEIALKEELFMK	2	0.9991
							LQLETEIALKEELFMKK	4	0.8827
							QAQYEALLNIK	2	0.9988
							QSVENDIHLR	2	0.9845
							QSVENDIHLR	3	0.9375
							SAEVGAETTLTLR	2	0.9467
							TVQSLEIDLSMR	2	0.9996
							VIDDTNTR	2	0.9987
							VKLGAETATYR	2	0.904
							VKYETELAMR	2	0.9632
							VKYETELAMR	3	0.9919
							YALQMEQLNGILLHSELAQTR	3	0.9993
Q5307-1	F8W543	F8W543_HUMAN	NAP11	Nucleosome assembly protein 1-like 1	1.0000	6.4	2	2	4
Q5307-2	HOYH88	HOYH88_HUMAN	NAP11	Nucleosome assembly protein 1-like 1 (Fragment)	1.0000	11.86	2	2	4
							FYEEVDLDR	2	0.9994
							GIPEFWLTVFK	2	0.9985
Q5308-1	F8W646	F8W646_HUMAN	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	1.0000	40.38	5	5	11
							EDSORPPGAHLTVK	2	0.9891
							KLFIGGLSFETDESIR	2	0.9997
							LFIGGLSFETDESIR	2	0.9997
							SESPKEFQLR	2	0.9968
							SHEFGWGLTDCVVMRDPNTRK	4	0.9856
Q5309-1	F8W617	F8W617_HUMAN	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	1.0000	23.78	6	6	13
Q5309-2	P09651	ROA1_HUMAN	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	1.0000	19.62	6	6	13
Q5309-3	P09651-3	ROA1_HUMAN	HNRNPA1	isoform 2 of Heterogeneous nuclear ribonucleoprotein A1	1.0000	27.34	6	6	13
Q5309-4	P09651-2	ROA1_HUMAN	HNRNPA1	isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	1.0000	22.81	6	6	13
							EDSORPPGAHLTVK	2	0.9891
							IEVIEIMTOR	2	0.9984
							KLFIGGLSFETDESIR	2	0.9997
							LFIGGLSFETDESIR	2	0.9997
							SESPKEFQLR	2	0.9968
							SHEFGWGLTDCVVMRDPNTRK	4	0.9856
Q5310-1	P35580-2	MYH10_HUMAN	MYH10	isoform 2 of Myosin-10	1.0000	5.82	8	10	18
Q5310-2	P35580-3	MYH10_HUMAN	MYH10	isoform 3 of Myosin-10	1.0000	5.81	8	10	18
Q5310-3	P35580-4	MYH10_HUMAN	MYH10	isoform 4 of Myosin-10	1.0000	5.78	8	10	18
Q5310-4	P35580-5	MYH10_HUMAN	MYH10	isoform 5 of Myosin-10	1.0000	5.84	8	10	18
Q5310-5	F8W6L6	F8W6L6_HUMAN	MYH10	Myosin-10	1.0000	5.82	8	10	18
Q5310-6	P35580	MYH10_HUMAN	MYH10	Myosin-10	1.0000	5.87	8	10	18
							ADEWLKM	2	0.9937
							AGVLAHLEER	2	0.9993
							DKADFCIHYAGK	3	0.8934
							LDPHLVLDQLR	2	0.9489
							LDPHLVLDQLR	3	0.9995
							LQQLFNHTMFILEQEYQR	3	0.9995
							SLEAEILQLEELASSER	2	0.9997
							SLEAEILQLEELASSER	3	0.955
							TQLEELDELQATEDAK	2	0.9997
							VEDMAELTCLINEASVYHNLK	3	0.9921
Q5311-1	P02751	FINC_HUMAN	FN1	Fibronectin	1.0000	5.74	10	10	18
Q5311-2	P02751-10	FINC_HUMAN	FN1	isoform 10 of Fibronectin	1.0000	6.3	10	10	18
Q5311-3	P02751-11	FINC_HUMAN	FN1	isoform 11 of Fibronectin	1.0000	5.74	10	10	18
Q5311-4	P02751-12	FINC_HUMAN	FN1	isoform 12 of Fibronectin	1.0000	6.82	10	10	18
Q5311-5	P02751-13	FINC_HUMAN	FN1	isoform 13 of Fibronectin	1.0000	6.04	10	10	18
Q5311-6	P02751-14	FINC_HUMAN	FN1	isoform 14 of Fibronectin	1.0000	6.05	10	10	18
Q5311-7	P02751-15	FINC_HUMAN	FN1	isoform 15 of Fibronectin	1.0000	5.53	10	10	18
Q5311-8	P02751-17	FINC_HUMAN	FN1	isoform 17 of Fibronectin	1.0000	5.88	10	10	18
Q5311-9	P02751-3	FINC_HUMAN	FN1	isoform 3 of Fibronectin	1.0000	5.82	10	10	18
Q5311-10	P02751-5	FINC_HUMAN	FN1	isoform 5 of Fibronectin	1.0000	6.2	10	10	18
Q5311-11	P02751-7	FINC_HUMAN	FN1	isoform 7 of Fibronectin	1.0000	5.6	10	10	18
Q5311-12	P02751-8	FINC_HUMAN	FN1	isoform 8 of Fibronectin	1.0000	5.97	10	10	18
Q5311-13	P02751-9	FINC_HUMAN	FN1	isoform 9 of Fibronectin	1.0000	6.12	10	10	18
Q5311-14	F8W7G7	F8W7G7_HUMAN	FN1	Ugi-Y3	1.0000	6.2	10	10	18
							DLQPFVETDVK	2	0.9906
							EYLGAICSTCFGGQR	2	0.9963
							SSPVVIDASTAIDAPSNLR	2	0.9995
							STTPDITGYR	2	0.8916
							SYTITGLQPGTDYK	2	0.9993
							TPYSCCTEGR	2	0.9808
							TYLGNALVCTCYGGSR	2	0.9967
							VPGTSTSATLTGLTR	2	0.9996
							VTDATETITISWR	2	0.9847
							WSRPQAPITGYR	3	0.8168
Q5312-1	F8W7I2	F8W7I2_HUMAN	PTGDS	Prostaglandin-H2 D-isomerase	1.0000	14.73	2	2	5
							AQGFTEDTIVLPQTDK	2	0.9996
							TMLLQPAGSLGSYSYR	2	0.9973
Q5313-1	F8W7I9	F8W7I9_HUMAN	RANGAP1	Ran GTPase-activating protein 1	1.0000	4.51	2	2	2
Q5313-2	HOY4Q3	HOY4Q3_HUMAN	RANGAP1	Ran GTPase-activating protein 1 (Fragment)	1.0000	9.49	2	2	2
							QVEVINFGDCILVR	2	0.9871
							SSACFTLQELK	2	0.9947
Q5314-1	F8W7L3	F8W7L3_HUMAN	A2M	Alpha-2-macroglobulin (Fragment)	1.0000	13.1	1	1	2
							SLFTDLEAENDVHCVAFVPK	3	0.999
Q5315-1	F8W810	F8W810_HUMAN		Uncharacterized protein	0.9995	2.58	1	1	1
Q5315-2	P41091	IF2G_HUMAN	EIF253	Eukaryotic translation initiation factor 2 subunit 3	0.9995	2.54	1	1	1
Q5315-3	Q2VIR3-2	IF2GL_HUMAN	EIF253L	isoform 2 of Putative eukaryotic translation initiation factor 2	0.9995	2.58	1	1	1
Q5315-4	Q2VIR3	IF2GL_HUMAN	EIF253L	Putative eukaryotic translation initiation factor 2 subunit 3-like	0.9995	2.54	1	1	1
							YNIYVECEYVK	2	0.9915
Q5316-1	G3XAM7	G3XAM7_HUMAN	CTNNA1	Catenin (C adherin-associated protein), alpha 1, 102kDa, isofo	1.0000	7.02	3	3	3
Q5316-2	F8W845	F8W845_HUMAN	CTNNA1	Catenin alpha-1	1.0000	7.35	3	3	3
Q5316-3	P35221	CTNA1_HUMAN	CTNNA1	Catenin alpha-1	1.0000	6.51	3	3	3
Q5316-4	P35221-2	CTNA1_HUMAN	CTNNA1	isoform 2 of Catenin alpha-1	1.0000	6.34	3	3	3
							LIEVANLACISISNNEGVK	2	0.9792
							MSASQLEALCPQVINAALAAKPSQK	3	0.9866
							QIIVDPLSFSEER	2	0.9465
Q5317-1	F8W9U3	F8W9U3_HUMAN	ABHD14B	Alpha/beta hydrolase domain-containing protein 14B	1.0000	16.35	4	5	10
							EALPGSGQAR	2	0.9926
							EGTIQVGGQALFFR	2	0.9994
							FSVLLHIGIR	2	0.9996
							FSVLLHIGIR	3	0.9984
							SVLLHIGIR	2	0.888
Q5318-1	F8WDD7	F8WDD7_HUMAN	ARPC4	Actin-related protein 2/3 complex subunit 4	1.0000	16.81	2	2	4

Q5318-2	P59998	ARPC4_HUMAN	ARPC4	Actin-related protein 2/3 complex subunit 4	1.0000	11.31	2	2	4
Q5318-3	P59998-2	ARPC4_HUMAN	ARPC4	Isoform 2 of Actin-related protein 2/3 complex subunit 4	1.0000	3.04	2	2	4
Q5318-4	P59998-3	ARPC4_HUMAN	ARPC4	Isoform 3 of Actin-related protein 2/3 complex subunit 4	1.0000	10.16	2	2	4
Q5318-5	F8WC6	F8WC6_HUMAN	ARPC4-TLL3	Protein ARPC4-TLL3	1.0000	10.5	2	2	4
				AENFRLR			2	0.9995	3
				VUEGSSNSVR			2	0.9947	1
Q5319-1	F8WC26	F8WC26_HUMAN	C15	Complement C15 subcomponent	1.0000	13.05	5	5	11
				DVVQITCLDGFVEVGR			2	0.9995	4
				GFQVVVTLR			2	0.9993	3
				LPVAPLR			2	0.972	1
				QFGPYCGHGFPPGLNIETK			3	0.9533	1
				SNALDIFQDLDTGQK			2	0.9978	2
Q5320-1	F8WE04	F8WE04_HUMAN	HSPB1	Heat shock protein beta-1	1.0000	13.98	2	2	11
				LFDQAFGLPR			2	0.9998	6
				VSLDVNHFAPELTVK			2	0.9997	5
Q5321-1	G3V1V0	G3V1V0_HUMAN	MYL6	Myosin light polypeptide 6	1.0000	61.49	8	10	18
				ALGQNPTNAEVLK			2	0.9994	2
				DQGTYYDYVEGLR			2	0.9909	2
				EAFQLFDR			2	0.9981	2
				HVLVTLGEEK			2	0.9993	1
				ILYSQCGDVMR			2	0.9992	1
				MTEEEVEMLVAGHEDSNGCINYEGR			3	0.8952	1
				NKQDGTYYDYVEGLR			2	0.9995	2
				NKQDGTYYDYVEGLR			3	0.9892	2
				VLDFEHLFPLMLQTVAK			2	0.9996	3
				VLDFEHLFPLMLQTVAK			3	0.9996	2
Q5322-1	G3V2W1	G3V2W1_HUMAN	SERPINA10	Protein Z-dependent protease inhibitor	0.9598	2.07	1	1	2
Q5322-2	Q9UK55	ZPI_HUMAN	SERPINA10	Protein Z-dependent protease inhibitor	0.9598	2.25	1	1	2
				LILVDYLFK			2	0.9598	2
Q5323-1	P42226-2	STAT6_HUMAN	STAT6	Isoform 2 of Signal transducer and activator of transcription 6	0.9255	2.38	1	1	1
Q5323-2	P42226-3	STAT6_HUMAN	STAT6	Isoform 3 of Signal transducer and activator of transcription 6	0.9255	2.17	1	1	1
Q5323-3	P42226	STAT6_HUMAN	STAT6	Signal transducer and activator of transcription 6	0.9255	1.89	1	1	1
Q5323-4	G3V2X7	G3V2X7_HUMAN	STAT6	Signal transducer and activator of transcription 6 (Fragment)	0.9255	10.39	1	1	1
				FSDSEIGGTTIAHVIR			3	0.9255	1
Q5324-1	Q86XR7-2	TICAM2_HUMAN	TICAM2	Isoform 2 of TIR domain-containing adapter molecule 2	0.9577	2.97	1	1	2
Q5324-2	Q9Y383-2	TMED7_HUMAN	TMED7	Isoform 2 of Transmembrane emp24 domain-containing protein 7	0.9577	6.38	1	1	2
Q5324-3	Q9Y383	TMED7_HUMAN	TMED7	Transmembrane emp24 domain-containing protein 7	0.9577	5.36	1	1	2
Q5324-4	G3V2Y2	G3V2Y2_HUMAN	TMED7	Transmembrane emp24 domain-containing protein 7 (Fragment)	0.9577	14.81	1	1	2
				QCIFYEDIAQGTK			2	0.9577	2
Q5325-1	G3V3A0	G3V3A0_HUMAN	SERPINA3	Alpha-1-antichymotrypsin	1.0000	30.24	6	6	16
				ADLSGITGAR			2	0.9993	3
				EIGELYLPK			2	0.9982	2
				FNRPLMIIVPTDQNIFFMSK			3	0.9991	5
				ITLTSALVETR			2	0.9997	3
				NLAWSQVAHK			2	0.9969	2
				TLLSALVETR			2	0.8869	1
Q5326-1	G3V3E1	G3V3E1_HUMAN	SKOR1	SKI family transcriptional corepressor 1	0.9976	6.8	2	2	2
Q5326-2	G3V5H7	G3V5H7_HUMAN	SKOR1	SKI family transcriptional corepressor 1	0.9976	6.72	2	2	2
Q5326-3	P84550	SKOR1_HUMAN	SKOR1	SKI family transcriptional corepressor 1	0.9976	6.53	2	2	2
				GEDGLTLDVTGTHLVEK			3	0.8056	1
				TFSLQGGGGGGANGSGGGGKGAGGGGGGGPGCGAEMAPGPPPHK			3	0.8299	1
Q5327-1	G3V453	G3V453_HUMAN	SAV1	Protein salvador homolog 1 (Fragment)	0.9418	11.69	1	1	1
				CASCLQTLR			2	0.9418	1
Q5328-1	G3V5I3	G3V5I3_HUMAN	SERPINA3	Alpha-1-antichymotrypsin (Fragment)	1.0000	51.11	2	2	5
				AAAATGTIFTR			2	0.9997	3
				AVVEVDEGSTR			2	0.9997	2
Q5329-1	Q6H9L7-3	ISM2_HUMAN	ISM2	Isoform 3 of Isthmin-2	0.9669	2.86	1	1	2
Q5329-2	Q6H9L7-5	ISM2_HUMAN	ISM2	Isoform 5 of Isthmin-2	0.9669	2.86	1	1	2
Q5329-3	G3XAI3	G3XAI3_HUMAN	ISM2	Isthmin-2	0.9669	2.9	1	1	2
Q5329-4	Q6H9L7	ISM2_HUMAN	ISM2	Isthmin-2	0.9669	2.45	1	1	2
				TRPCGYGCTATETR			2	0.9669	2
Q5330-1	P07225	PRO5_HUMAN	PRO51	Vitamin K-dependent protein 5	1.0000	29.17	17	21	46
				AHSCPSVWK			2	0.9907	1
				AHSCPSVWK			2	0.9996	3
				DVDECSLKPSICGTAVCK			2	0.9997	2
				DVDECSLKPSICGTAVCK			3	0.9937	1
				PSAEFDR			2	0.9947	1
				HCLVTVEK			2	0.9996	1
				IQALSLCSQQSH			2	0.975	2
				IQALSLCSQQSHLEF			2	0.986	2
				IQALSLCSQQSHLEFR			2	0.9997	3
				IQALSLCSQQSHLEFR			3	0.999	2
				ITTGDGVINGLWNVMVSELEHSISK			3	0.9861	1
				KVESELKPINPR			2	0.9997	2
				KVESELKPINPR			3	0.9985	2
				NGFVMSLKK			2	0.9966	2
				NNLELSTPLK			2	0.9975	2
				NNLELSTPLKTIETSHEDLQR			3	0.9994	3
				SLCSQQSHLEFR			2	0.9987	2
				SQDILLSVENTVIYR			2	0.9997	7
				SQDILLSVENTVIYR			3	0.9996	2
				VNRNNLELSTPLKTIETSHEDLQR			3	0.9976	3
				VYAFGEPR			2	0.9985	2
Q5331-1	G5E9G0	G5E9G0_HUMAN	RPL3	60S ribosomal protein L3	0.9999	8.83	2	2	3
				NNASTDYDLSK			2	0.8779	1
				SINPLGGFVHYGEVNTDFV			2	0.978	2
Q5332-1	G5E9J1	G5E9J1_HUMAN	SH3GLB2	Endophilin-B2	0.9978	45.83	1	1	1
				LASDAGIFTR			2	0.9884	1
Q5333-1	G5EA52	G5EA52_HUMAN	PDIA3	Protein disulfide-isomerase	1.0000	20	6	6	9
				EATNPPIVQEEKPK			2	0.9995	1
				ELSDFISYLQR			2	0.9994	2
				FISDKDASVGFDDSFSEAHSEFLK			3	0.9975	2
				LAPEYEAATR			2	0.9985	1
				LSKDPNVIK			2	0.9879	2
				TFSHELSDGFELESTAGEIPVVAIR			3	0.991	1
Q5334-1	G8IL88	G8IL88_HUMAN	APOL1	Apolipoprotein L1	0.9727	5.42	1	1	2
Q5334-2	O14791	APOL1_HUMAN	APOL1	Apolipoprotein L1	0.9727	3.77	1	1	2
Q5334-3	O14791-2	APOL1_HUMAN	APOL1	Isoform 2 of Apolipoprotein L1	0.9727	3.62	1	1	2
Q5334-4	O14791-3	APOL1_HUMAN	APOL1	Isoform 3 of Apolipoprotein L1	0.9727	3.95	1	1	2
				VTEPISAESGEQVER			2	0.9727	2
Q5335-1	P06060-2	MYL6_HUMAN	MYL6	Isoform Smooth muscle of Myosin light polypeptide 6	1.0000	65.56	8	10	20
Q5335-2	G8ILA2	G8ILA2_HUMAN	MYL6	Myosin light polypeptide 6	1.0000	65.13	8	10	20
				ALGQNPTNAEVLK			2	0.9994	2
				DQGTYYDYVEGLR			2	0.9909	2
				EAFQLFDR			2	0.9981	2
				HVLVTLGEEK			2	0.9993	1
				ILYSQCGDVMR			2	0.9992	1
				MTEEEVEMLVAGHEDSNGCINYEELVR			3	0.995	3
				NKQDGTYYDYVEGLR			2	0.9995	2
				NKQDGTYYDYVEGLR			3	0.9892	2
				VLDFEHLFPLMLQTVAK			2	0.9996	3
				VLDFEHLFPLMLQTVAK			3	0.9996	2
Q5336-1	G8ILD5	G8ILD5_HUMAN	DNM1L	Dynamin-1-like protein	0.9996	3.51	2	2	2
Q5336-2	O00429	DNM1L_HUMAN	DNM1L	Dynamin-1-like protein	0.9996	3.4	2	2	2
Q5336-3	O00429-3	DNM1L_HUMAN	DNM1L	Isoform 2 of Dynamin-1-like protein	0.9996	3.52	2	2	2
Q5336-4	O00429-4	DNM1L_HUMAN	DNM1L	Isoform 3 of Dynamin-1-like protein	0.9996	3.58	2	2	2
Q5336-5	O00429-2	DNM1L_HUMAN	DNM1L	Isoform 4 of Dynamin-1-like protein	0.9996	3.45	2	2	2
Q5336-6	O00429-5	DNM1L_HUMAN	DNM1L	Isoform 5 of Dynamin-1-like protein	0.9996	3.52	2	2	2
Q5336-7	O00429-6	DNM1L_HUMAN	DNM1L	Isoform 6 of Dynamin-1-like protein	0.9996	3.34	2	2	2
Q5336-8	O00429-8	DNM1L_HUMAN	DNM1L	Isoform 8 of Dynamin-1-like protein	0.9996	3.39	2	2	2
				ALQGASQIAEIR			2	0.9843	1
				VIETSEICGGAR			2	0.9722	1
Q5337-1	HOY300	HOY300_HUMAN	HP	Haptoglobin	1.0000	15.16	4	4	9

Q5337-2	J3QR68	J3QR68_HUMAN	HP	Haptoglobin (Fragment)	1.0000	16.58	4	4	9
						IAPTLTYVVK	2	0.909	1
						SCAVAEYGVYVK	2	0.9997	4
						VTSIQDWVQK	2	0.9993	2
						YQEDTCYDAGSAFAVHLEEDTWTATGILSFDK	3	0.9973	2
Q5338-1	HOY3H6	HOY3H6_HUMAN	C2	Complement C2b fragment (Fragment)	1.0000	8.37	3	3	7
Q5338-2	P06681-2	CO2_HUMAN	C2	Isoform 2 of Complement C2	1.0000	8.18	3	3	7
Q5338-3	P06681-3	CO2_HUMAN	C2	Isoform 3 of Complement C2	1.0000	7.1	3	3	7
						CSNVLVTGSSER	2	0.9988	3
						EVVTDQFLCSGTQDESQCKGSGGAVFLER	3	0.9981	3
						GESGGAVFLER	2	0.8935	1
Q5339-1	HOY482	HOY482_HUMAN	EPB41L1	Band 4.1-like protein 1 (Fragment)	1.0000	16.81	1	1	1
Q5339-2	Q9H4G0-3	E41L1_HUMAN	EPB41L1	Isoform 3 of Band 4.1-like protein 1	1.0000	2.59	1	1	1
						IIITGDEDVDQDALAIK	2	0.9979	1
Q5340-1	HOY494	HOY494_HUMAN	SIK3	Serine/threonine-protein kinase SIK3	0.9576	1.98	1	1	1
Q5340-2	J3KPC8	J3KPC8_HUMAN	SIK3	Serine/threonine-protein kinase SIK3	0.9576	1.89	1	1	1
						MAAAASGAGGAGAGTGAGPAGR	3	0.8051	1
Q5341-1	P12268	IMDH2_HUMAN	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	1.0000	12.84	5	6	8
Q5341-2	HOY4R1	HOY4R1_HUMAN	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2 (Fragment)	1.0000	14.04	5	6	8
						DIDFLKEEHDCFLIEIMTK	3	0.9155	1
						HGFCGPITDTGR	2	0.9992	1
						LVGISSR	2	0.996	1
						NLIDAGVDALR	2	0.9869	1
						REDLVVAPAGITLK	2	0.9996	2
						REDLVVAPAGITLK	3	0.998	2
Q5342-1	P41222	PTGDS_HUMAN	PTGDS	Prostaglandin-H2 D-isomerase	1.0000	32.63	3	3	7
Q5342-2	HOY5A1	HOY5A1_HUMAN	PTGDS	Prostaglandin-H2 D-isomerase (Fragment)	1.0000	29.11	3	3	7
						AQGFTEDTIVLPQTDK	2	0.9996	3
						SPHWGSTYSVSVVETDYDQYALLYSGSK	3	0.9717	2
						TMLLPAGSLGGSYSYR	2	0.9973	2
Q5343-1	HOY5D1	HOY5D1_HUMAN	C15	Complement C15 subcomponent (Fragment)	1.0000	16.9	4	4	9
						GFGVYVTLR	2	0.9993	3
						QFGPYCGHGPPLNIETK	3	0.9533	1
						SNALDIFQDITGQK	2	0.9978	2
						SWDIEVPEGYGIHLVF	2	0.9818	3
Q5344-1	HOY626	HOY626_HUMAN		Uncharacterized protein	1.0000	2.62	2	2	3
Q5344-2	K7EL43	K7EL43_HUMAN	TRIM16	Tripartite motif-containing protein 16 (Fragment)	1.0000	13.59	2	2	3
						AVAEMQFGEELAAVR	2	0.9994	1
						SVLVSVSEVK	2	0.9846	2
Q5345-1	HOY630	HOY630_HUMAN	STK24	Serine/threonine-protein kinase 24 12 kDa subunit (Fragment)	1.0000	20.05	5	6	12
						AANVLSEHGEVK	2	0.9963	1
						ADIWSLGITAIELAR	2	0.9997	3
						ADIWSLGITAIELAR	3	0.9996	2
						GAIYLAEEACPGISDITVAQLVQR	3	0.9952	2
						SQACGGNLSGSEELR	2	0.9997	3
						VLFLPK	2	0.9889	1
Q5346-1	Q6ZNU1-2	NBE12_HUMAN	NBEAL2	Isoform 2 of Neurobeachin-like protein 2	0.9885	0.74	1	1	1
Q5346-2	Q6ZNU1-3	NBE12_HUMAN	NBEAL2	Isoform 3 of Neurobeachin-like protein 2	0.9885	0.7	1	1	1
Q5346-3	Q6ZNU1	NBE12_HUMAN	NBEAL2	Neurobeachin-like protein 2	0.9885	0.69	1	1	1
Q5346-4	HOY764	HOY764_HUMAN	NBEAL2	Neurobeachin-like protein 2 (Fragment)	0.9885	0.93	1	1	1
						CPSLSEPPSSCCIGSAGYR	2	0.9802	1
Q5347-1	HOY7N1	HOY7N1_HUMAN	DDAH2	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment)	1.0000	22.87	4	5	8
Q5347-2	Q5SRR8	Q5SRR8_HUMAN	DDAH2	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment)	1.0000	18.22	4	5	8
Q5347-3	Q5SSV3	Q5SSV3_HUMAN	DDAH2	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment)	1.0000	19.03	4	5	8
						DFAVSTVPVSGPSHLR	2	0.9996	3
						DFAVSTVPVSGPSHLR	3	0.9982	1
						EPFVGLSK	2	0.9809	1
						GAEVADTTR	2	0.9885	2
						KALQDLGLR	2	0.9989	1
Q5348-1	HOY8W2	HOY8W2_HUMAN	GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)	1.0000	12.77	3	3	3
						DVLSVAFSSDNR	2	0.983	1
						LWDLTTGTTTR	2	0.938	1
						YWLCAATGPSIK	2	0.9997	1
Q5349-1	HOY9Q1	HOY9Q1_HUMAN	LAP3	Cytosol aminopeptidase (Fragment)	1.0000	5.77	1	1	2
						GVLFASQGNLAR	2	0.9994	2
Q5350-1	P03952	KLKB1_HUMAN	KLKB1	Plasma kallikrein	1.0000	5.64	3	3	7
Q5350-2	HOYAC1	HOYAC1_HUMAN	KLKB1	Plasma kallikrein heavy chain (Fragment)	1.0000	5.25	3	3	7
						EIIHQNYK	2	0.8833	1
						IAYGTGGSGYSRLR	2	0.9994	2
						LVGITSWEGGCAR	2	0.9977	4
Q5351-1	J3KPE3	J3KPE3_HUMAN	GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)	1.0000	16.12	4	4	5
Q5351-2	HOYAF8	HOYAF8_HUMAN	GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment)	1.0000	22.22	4	4	5
						DVLSVAFSSDNR	2	0.983	1
						LWDLTTGTTTR	2	0.938	1
						VWQVTIGTR	2	0.9992	2
						YWLCAATGPSIK	2	0.9997	1
Q5352-1	P60228	EIF3E_HUMAN	EIF3E	Eukaryotic translation initiation factor 3 subunit E	1.0000	9.44	3	3	5
Q5352-2	HOYBR5	HOYBR5_HUMAN	EIF3E	Eukaryotic translation initiation factor 3 subunit E (Fragment)	1.0000	24.56	3	3	5
						HLVPLLEFLSVK	3	0.9994	3
						LDLSDTNMVDAMDVYK	2	0.9754	1
						QLQAEIPEYK	2	0.9295	1
Q5353-1	P04233	HG2A_HUMAN	CD74	HLA class II histocompatibility antigen gamma chain	0.9765	6.42	1	1	3
Q5353-2	HOYB22	HOYB22_HUMAN	CD74	HLA class II histocompatibility antigen gamma chain (Fragment)	0.9765	6.01	1	1	3
						CQEEVSHIPAVHPGSRPK	3	0.9765	3
Q5354-1	HOYB82	HOYB82_HUMAN	NAGK	N-acetyl-D-glucosamine kinase (Fragment)	1.0000	19.05	1	1	2
Q5354-2	HOYB87	HOYB87_HUMAN	NAGK	N-acetyl-D-glucosamine kinase (Fragment)	1.0000	8.79	1	1	2
						SLGLSLSGDQDQEDAGR	2	0.9996	2
Q5355-1	H7C286	H7C286_HUMAN	NAGK	N-acetyl-D-glucosamine kinase	0.9997	5.61	1	1	1
Q5355-2	HOYF44	HOYF44_HUMAN	NAGK	N-acetyl-D-glucosamine kinase (Fragment)	0.9997	10.09	1	1	1
						EGFLLALTQGR	2	0.8813	1
Q5356-1	HOYFH3	HOYFH3_HUMAN	C1R	Complement C1r subcomponent	1.0000	7.5	3	3	8
Q5356-2	P00736	C1R_HUMAN	C1R	Complement C1r subcomponent	1.0000	6.95	3	3	8
						LPVANPQACENWLR	2	0.9983	3
						LVFQDFLEPSEGCFYDVYK	2	0.9993	3
						WVATGVSVWGCSR	2	0.9985	2
Q5357-1	HOYFX9	HOYFX9_HUMAN	H2AFJ	Histone H2A (Fragment)	1.0000	20.65	2	2	5
						AVLEYLTAEILELAGNAAR	3	0.9888	3
						VLEYLTAEILELAGNAAR	3	0.9791	2
Q5358-1	HOYG07	HOYG07_HUMAN	MLEC	Malectin (Fragment)	0.9999	6.94	1	1	3
						FAEVYFAQSQKQ	2	0.9992	3
Q5359-1	Q8NE71	ABCF1_HUMAN	ABCF1	ATP-binding cassette sub-family F member 1	1.0000	4.14	3	3	3
Q5359-2	HOYGW7	HOYGW7_HUMAN	ABCF1	ATP-binding cassette sub-family F member 1 (Fragment)	1.0000	5.87	3	3	3
Q5359-3	Q8NE71-2	ABCF1_HUMAN	ABCF1	Isoform 2 of ATP-binding cassette sub-family F member 1	1.0000	4.34	3	3	3
						FGLESHAHTIQICK	3	0.9329	1
						GAVIVVSHDAR	2	0.9994	1
						STLLLLTGK	2	0.999	1
Q5360-1	HOYH81	HOYH81_HUMAN	ATP5B	ATP synthase subunit beta (Fragment)	1.0000	7.46	2	2	6
						FTQAGSEVSALLGR	2	0.9997	3
						VALTGTLVAYFR	2	0.9991	3
Q5361-1	HOYHR8	HOYHR8_HUMAN	NTSC2	Cytosolic purine 5'-nucleotidase (Fragment)	1.0000	8.28	1	1	3
Q5361-2	Q5JUV3	Q5JUV3_HUMAN	NTSC2	Cytosolic purine 5'-nucleotidase (Fragment)	1.0000	7.47	1	1	3
						GLVFDLYGNLLK	2	0.9997	3
Q5362-1	HOYI43	HOYI43_HUMAN	MYL6	Myosin light polypeptide 6 (Fragment)	1.0000	37.35	2	2	3
						NKDQGTEDYVEGLR	2	0.9995	2
						VFDKEGNGTVMGAIR	3	0.84	1
Q5363-1	HOYJ11	HOYJ11_HUMAN	ACTN1	Alpha-actinin-1 (Fragment)	1.0000	11.59	2	2	5
Q5363-2	HOYJW3	HOYJW3_HUMAN	ACTN1	Alpha-actinin-1 (Fragment)	1.0000	9.56	2	2	5
Q5363-3	H7C5W8	H7C5W8_HUMAN	ACTN1	Alpha-actinin-1 (Fragment)	1.0000	8.08	2	2	5
						TINEVENQLTR	2	0.999	2
						VGVWQQLTTIAR	2	0.9996	3
Q5364-1	HOYJ21	HOYJ21_HUMAN	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1 (Fragment)	1.0000	5.56	1	1	2
						VTFVNFVTTR	2	0.9992	2
Q5365-1	HOYMU9	HOYMU9_HUMAN	ANXA2	Annexin	1.0000	17.39	3	4	6

Q5365-2	HOYK54	HOYK54_HUMAN	ANKA2	Annexin (Fragment)	1.0000	22.73	3	4	6
Q5365-3	HOYMD0	HOYMD0_HUMAN	ANKA2	Annexin (Fragment)	1.0000	17.62	3	4	6
Q5365-4	HOYMM1	HOYMM1_HUMAN	ANKA2	Annexin (Fragment)	1.0000	26.85	3	4	6
Q5365-5	HOYN42	HOYN42_HUMAN	ANKA2	Annexin (Fragment)	1.0000	15.63	3	4	6
Q5365-6	P07355	ANKA2_HUMAN	ANKA2	Annexin A2	1.0000	11.8	3	4	6
Q5365-7	P07355-2	ANKA2_HUMAN	ANKA2	Isoform 2 of Annexin A2	1.0000	11.2	3	4	6
						GLTDFDSLIEICSR	2	0.9937	1
						GVDEVTVNLTNR	2	0.9994	2
						GVDEVTVNLTNR	3	0.9926	1
						TNQLDEINR	2	0.9962	2
Q5366-1	HOYLE8	HOYLE8_HUMAN	IQGAP1	Ras GTPase-activating-like protein IQGAP1	1.0000	3.41	3	3	6
						EELQSSISGVTAAYNR	2	0.9997	2
						EQLWLANGLITR	2	0.9995	3
						RLIVDVIR	2	0.996	1
Q5367-1	HOYLF3	HOYLF3_HUMAN	B2M	Beta-2-microglobulin form pl 5.3 (Fragment)	1.0000	18.31	1	1	3
						IEKVEHSOLFSK	2	0.9993	3
Q5368-1	HOYN26	HOYN26_HUMAN	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member 1	1.0000	53.67	7	9	15
Q5368-2	P39687	ANP32A_HUMAN	ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member 1	1.0000	38.15	7	9	15
						CPNLTHNLISGNK	2	0.9996	1
						CPNLTHNLISGNK	3	0.9195	1
						ELVDNSR	2	0.99	1
						KLISLSDNR	2	0.993	1
						SLDLFNCVTLNDYR	2	0.9997	4
						SLDLFNCVTLNDYR	3	0.9929	2
						SLDLFNCVTLNDYRNVFK	3	0.9812	1
						SNEGKLGLTDFEELFLSTINVLTSIANLPK	3	0.9988	1
						VSGGLEVLAEKCPNLTHNLISGNK	3	0.9939	3
Q5369-1	H3BNA2	H3BNA2_HUMAN	CORO1A	Coronin (Fragment)	1.0000	10.81	1	1	3
Q5369-2	H3BRJ0	H3BRJ0_HUMAN	CORO1A	Coronin (Fragment)	1.0000	6.43	1	1	3
Q5369-3	H3BSL1	H3BSL1_HUMAN	CORO1A	Coronin (Fragment)	1.0000	7.34	1	1	3
Q5369-4	H3BTU6	H3BTU6_HUMAN	CORO1A	Coronin (Fragment)	1.0000	6.5	1	1	3
Q5369-5	H3BU76	H3BU76_HUMAN	CORO1A	Coronin (Fragment)	1.0000	9.7	1	1	3
						VSQTTWDSGFCVNPVK	2	0.9995	3
Q5370-1	P15170	ERF3A_HUMAN	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit 1	1.0000	9.02	4	4	4
Q5370-2	H3BR35	H3BR35_HUMAN	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit 1	1.0000	9.47	4	4	4
Q5370-3	P15170-2	ERF3A_HUMAN	GSPT1	Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit 1	1.0000	7.08	4	4	4
Q5370-4	P15170-3	ERF3A_HUMAN	GSPT1	Isoform 3 of Eukaryotic peptide chain release factor GTP-binding subunit 1	1.0000	7.06	4	4	4
						AYFETKK	2	0.9461	1
						ETWYLSWALDTNQEER	2	0.9474	1
						HFTILDAPGHK	3	0.998	1
						KGEFETGFEK	2	0.9855	1
Q5371-1	H3BRG4	H3BRG4_HUMAN	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	0.9844	3.88	1	1	2
Q5371-2	P22695	QCR2_HUMAN	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	0.9844	3.53	1	1	2
						THAQGNLSMTDVQAAK	2	0.9844	2
Q5372-1	H3BRY3	H3BRY3_HUMAN	CORO1A	Coronin	1.0000	12.34	4	4	9
Q5372-2	P31146	CORO1A_HUMAN	CORO1A	Coronin-1A	1.0000	10.41	4	4	9
						DGGUICSCR	2	0.9895	2
						ILTTGFSR	2	0.9611	1
						VSQTTWDSGFCVNPVK	2	0.9995	3
						YFEITSEAPLHYL	2	0.9917	3
Q5373-1	H3BSV8	H3BSV8_HUMAN	GSPT1	Eukaryotic peptide chain release factor GTP-binding subunit 1	1.0000	5.53	1	1	1
						HFTILDAPGHK	3	0.998	1
Q5374-1	H3BVG3	H3BVG3_HUMAN	JMJD8	JmjC domain-containing protein 8	0.9577	12.79	1	1	1
Q5374-2	Q96516	JMJD8_HUMAN	JMJD8	JmjC domain-containing protein 8	0.9577	8.38	1	1	1
						ADLTAEFVQVQYAFVRPVILQGLTNSR	3	0.9269	1
Q5375-1	H7BKV5	H7BKV5_HUMAN	COL18A1	Endostatin (Fragment)	1.0000	5.39	2	2	4
Q5375-2	H7CA57	H7CA57_HUMAN	COL18A1	Endostatin (Fragment)	1.0000	13.21	2	2	4
						LTSEYCEWTR	2	0.993	1
						QAMLGQVHVEPGWLUFVQEELVVR	3	0.9986	3
Q5376-1	H7BY16	H7BY16_HUMAN	NCL	Nucleolin (Fragment)	1.0000	6.08	2	2	3
						EVFEDAAEIR	2	0.9996	2
						GIAYIEFK	2	0.9995	1
Q5377-1	H7COL5	H7COL5_HUMAN	ITI4	35 kDa inter-alpha-trypsin inhibitor heavy chain H4 (Fragment)	1.0000	4.31	2	2	9
						AGFSWIEVTFK	2	0.9994	4
						RLDYQEGPPGVEISCSVEL	2	0.9995	5
Q5378-1	P47897	SYQ_HUMAN	QARS	Glutamine-tRNA ligase	1.0000	7.48	5	5	7
Q5378-2	H7COR3	H7COR3_HUMAN	QARS	Glutamine-tRNA ligase (Fragment)	1.0000	22.92	5	5	7
Q5378-3	P47897-2	SYQ_HUMAN	QARS	Isoform 2 of Glutamine-tRNA ligase	1.0000	5.59	5	5	7
						AMAVLIESLR	2	0.9991	2
						GFHOVFAPAPFIER	3	0.999	2
						GPSGCVESLEYTCR	2	0.9994	1
						LAWGQPVQLR	2	0.9993	1
						VIITNPPAAK	2	0.9755	1
Q5379-1	H7C1L7	H7C1L7_HUMAN	NAGK	N-acetyl-D-glucosamine kinase	1.0000	16.98	2	2	3
						SEVLVSEDGK	2	0.9586	1
						SLGLSLSGDDQEDAGR	2	0.9996	2
Q5380-1	Q99460	PSMD1_HUMAN	PSMD1	26S proteasome non-ATPase regulatory subunit 1	0.9872	1.26	1	1	3
Q5380-2	H7C378	H7C378_HUMAN	PSMD1	26S proteasome non-ATPase regulatory subunit 1 (Fragment)	0.9872	6.25	1	1	3
Q5380-3	Q99460-2	PSMD1_HUMAN	PSMD1	Isoform 2 of 26S proteasome non-ATPase regulatory subunit 1	0.9872	1.3	1	1	3
						AAVESLGLIFR	2	0.9872	3
Q5381-1	H7C3G9	H7C3G9_HUMAN	NAGK	N-acetyl-D-glucosamine kinase	1.0000	6.47	2	2	2
Q5381-2	Q9UJ70	NAGK_HUMAN	NAGK	N-acetyl-D-glucosamine kinase	1.0000	6.4	2	2	2
						EGFLALTOGR	2	0.8813	1
						SEVLVSEDGK	2	0.9586	1
Q5382-1	Q15083	ERC2_HUMAN	ERC2	ERC protein 2	0.9855	1.15	1	1	1
Q5382-2	H7C4G9	H7C4G9_HUMAN	ERC2	ERC protein 2 (Fragment)	0.9855	2.08	1	1	1
						KESELLALQTK	2	0.8485	1
Q5383-1	Q9NQ84	NIT2_HUMAN	NIT2	Omega-amidase NIT2	0.9939	8.33	2	2	2
Q5383-2	H7C579	H7C579_HUMAN	NIT2	Omega-amidase NIT2 (Fragment)	0.9939	8.68	2	2	2
						FAELAQIYAGR	2	0.9573	1
						LALQLQISSIK	2	0.8575	1
Q5384-1	Q7K2F4	SND1_HUMAN	SND1	Staphylococcal nuclease domain-containing protein 1	0.9482	1.43	1	1	1
Q5384-2	H7C597	H7C597_HUMAN	SND1	Staphylococcal nuclease domain-containing protein 1 (Fragment)	0.9482	5.63	1	1	1
						SEAVVEYVSGSR	2	0.9482	1
Q5385-1	H7CSR1	H7CSR1_HUMAN	CP	Ceruloplasmin (Fragment)	1.0000	4.46	3	4	5
						EVGPTNADPVLAK	2	0.9281	1
						EYTDASFTRNK	2	0.9964	2
						GAYPLSIEPIGR	2	0.9988	2
Q5386-1	P16615-2	AT2A2_HUMAN	ATP2A2	Isoform 2 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1.0000	2.81	2	2	3
Q5386-2	P16615-3	AT2A2_HUMAN	ATP2A2	Isoform 3 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1.0000	2.8	2	2	3
Q5386-3	P16615-4	AT2A2_HUMAN	ATP2A2	Isoform 4 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1.0000	2.76	2	2	3
Q5386-4	P16615-5	AT2A2_HUMAN	ATP2A2	Isoform 5 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1.0000	2.81	2	2	3
Q5386-5	P16615	AT2A2_HUMAN	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1.0000	2.69	2	2	3
Q5386-6	H7C5W9	H7C5W9_HUMAN	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (Fragment)	1.0000	3	2	2	3
						IGIFGQDEDVTSK	2	0.9946	1
						VGEATETALTCLVEK	2	0.9992	2
Q5387-1	H9KV48	H9KV48_HUMAN	SERPING1	Plasma protease C1 inhibitor	1.0000	20.73	11	12	28
						DFTCVHQALK	2	0.9995	1
						FOPTLTILPR	2	0.9458	1
						GVTSVSIQFHSPDLAIR	2	0.9997	3
						GVTSVSIQFHSPDLAIR	3	0.995	1
						LLDLSPSDR	2	0.9988	4
						LVLNAYLSAK	2	0.9996	3
						TLLVFEVQQPF	2	0.9254	1
						TLLVFEVQQPLF	2	0.9916	2
						TLLVFEVQQPLF	2	0.9859	3
						TNLSLSYPK	2	0.9995	4
						TNLSLSYPKDFTCVHQALK	3	0.9887	2
						VTSQDMLSIMEK	2	0.9994	3
Q5388-1	H9KV70	H9KV70_HUMAN	LCN2	Neutrophil gelatinase-associated lipocalin	1.0000	33	4	4	9
Q5388-2	P80188	NGAL_HUMAN	LCN2	Neutrophil gelatinase-associated lipocalin	1.0000	33.33	4	4	9
Q5388-3	X6R8F3	X6R8F3_HUMAN	LCN2	Neutrophil gelatinase-associated lipocalin	1.0000	33	4	4	9
						SLGLPENHFPVPIDQCIDG	2	0.9871	1

						TFVPGCQGEFTLGNIK	2	0.9962	2
						VPLQNFQDNQFGQK	2	0.9996	2
						WYVVLGNAILR	2	0.9994	4
Q5389-1	H9KV75	H9KV75_HUMAN	ACTN1	Alpha-actinin-1	1.0000	8.39	6	6	12
Q5389-2	P12814	ACTN1_HUMAN	ACTN1	Alpha-actinin-1	1.0000	7.74	6	6	12
Q5389-3	P12814-2	ACTN1_HUMAN	ACTN1	Isoform 2 of Alpha-actinin-1	1.0000	7.78	6	6	12
Q5389-4	P12814-3	ACTN1_HUMAN	ACTN1	Isoform 3 of Alpha-actinin-1	1.0000	7.55	6	6	12
Q5389-5	P12814-4	ACTN1_HUMAN	ACTN1	Isoform 4 of Alpha-actinin-1	1.0000	7.42	6	6	12
						EGLLWYCOR	2	0.9195	1
						FAIDQSVETSAS	2	0.9893	1
						LAILGHNVEYSK	2	0.9787	2
						LASDLLEWIR	2	0.9974	3
						TINEVENQILTR	2	0.999	2
						VGWEQLLTIIAR	2	0.9996	3
Q5390-1	H9KV83	H9KV83_HUMAN	OTOG	Otogelin	0.9980	0.74	2	2	2
Q5390-2	Q6ZRI0	OTOG_HUMAN	OTOG	Otogelin	0.9980	0.72	2	2	2
						DLAACCG	2	0.9532	1
						VGGSVVPVLEGCCR	3	0.9581	1
Q5391-1	I3L168	I3L168_HUMAN	MYO1C	Unconventional myosin-Ic (Fragment)	1.0000	10.45	1	1	2
Q5391-2	I3L204	I3L204_HUMAN	MYO1C	Unconventional myosin-Ic (Fragment)	1.0000	5.24	1	1	2
Q5391-3	I3L3F5	I3L3F5_HUMAN	MYO1C	Unconventional myosin-Ic (Fragment)	1.0000	10.22	1	1	2
Q5391-4	I3L3Y6	I3L3Y6_HUMAN	MYO1C	Unconventional myosin-Ic (Fragment)	1.0000	8.24	1	1	2
Q5391-5	I3L4D4	I3L4D4_HUMAN	MYO1C	Unconventional myosin-Ic (Fragment)	1.0000	8.54	1	1	2
						LLQFYAETCPAPER	2	0.9986	2
Q5392-1	I3L3Y0	I3L3Y0_HUMAN	KIAA0753	Uncharacterized protein KIAA0753	0.9610	2.82	1	1	1
Q5392-2	Q2KHM9	K0753_HUMAN	KIAA0753	Uncharacterized protein KIAA0753	0.9610	0.72	1	1	1
Q5392-3	I3L2A7	I3L2A7_HUMAN	KIAA0753	Uncharacterized protein KIAA0753 (Fragment)	0.9610	10.14	1	1	1
						SLLVQVR	2	0.961	1
Q5393-1	I3L2G1	I3L2G1_HUMAN	NSF	Vesicle-fusing ATPase (Fragment)	0.9961	12.5	2	2	2
Q5393-2	K7EQD6	K7EQD6_HUMAN	NSF	Vesicle-fusing ATPase (Fragment)	0.9961	9.44	2	2	2
						KAPPGGR	2	0.961	1
						LLDVRVIGPR	3	0.8999	1
Q5394-1	Q96N8-2	NEUL4_HUMAN	NEURL4	Isoform 2 of Neuralized-like protein 4	0.9994	3.91	1	1	2
Q5394-2	I3L2W2	I3L2W2_HUMAN	NEURL4	Neuralized-like protein 4	0.9994	3.97	3	4	4
Q5394-3	Q96N8	NEUL4_HUMAN	NEURL4	Neuralized-like protein 4	0.9994	3.91	3	4	4
						AAGSGSGSGSGGPGPGPGGGGGPSGSGSGPGSNGGLSGGGELHPR	3	0.9851	1
						AAGSGSGSGSGGPGPGPGGGGGPSGSGSGPGSNGGLSGGGELHPR	4	0.9046	1
						AAGSGSGSGSGGPGPGPGGGGGPSGSGSGPGSNGGLSGGGELHPRTR	3	0.9258	1
						VGVERTVAGELR	3	0.9128	1
Q5395-1	I3L312	I3L312_HUMAN	P4HB	Protein disulfide-isomerase (Fragment)	1.0000	34.13	5	6	10
						DAPEEDHVLVLR	2	0.9576	2
						KSNFAEALAANK	3	0.9852	1
						QFLQAAEAIDIPFGITSNDVFSK	3	0.9986	1
						THILLPLK	2	0.9987	2
						THILLPLK	3	0.9996	2
						YQLDKQGVLFK	3	0.9983	2
Q5396-1	I3L3B0	I3L3B0_HUMAN	C10BP	Complement component 1 Q subcomponent-binding protein	0.9927	16.85	1	1	4
Q5396-2	Q07021	C10BP_HUMAN	C10BP	Complement component 1 Q subcomponent-binding protein	0.9927	10.64	1	1	4
Q5396-3	I3L3Q7	I3L3Q7_HUMAN	C10BP	Complement component 1 Q subcomponent-binding protein	0.9927	16.95	1	1	4
						GVDNTFADELVELSTALEHQEYTFLEDLK	3	0.9927	4
Q5397-1	I3L3P5	I3L3P5_HUMAN	P4HB	Protein disulfide-isomerase (Fragment)	1.0000	10.26	1	1	2
						VDATESDLAQYGVVR	2	0.9997	2
Q5398-1	I3L501	I3L501_HUMAN	MYO1C	Unconventional myosin-Ic (Fragment)	1.0000	14.29	2	2	3
						LLQFYAETCPAPER	2	0.9986	2
						VTMESALTAR	2	0.9769	1
Q5399-1	J3KNB4	J3KNB4_HUMAN	CAMP	Cathelicidin antimicrobial peptide	0.9952	5.2	1	1	3
Q5399-2	P49913	CAMP_HUMAN	CAMP	Cathelicidin antimicrobial peptide	0.9952	5.29	1	1	3
						FALLGDOFFR	2	0.993	3
Q5400-1	J3KNC0	J3KNC0_HUMAN	GTF2A1	Transcription initiation factor IIA beta chain	0.9692	18.64	1	1	2
Q5400-2	P52655	TF2AA_HUMAN	GTF2A1	Transcription initiation factor IIA subunit 1	0.9692	2.93	1	1	2
						SVIEDVINDVR	2	0.9692	2
Q5401-1	P68402	PA1B2_HUMAN	PAFAH1B2	Platelet-activating factor acetylhydrolase IB subunit beta	0.9488	3.93	1	1	1
Q5401-2	J3KNE3	J3KNE3_HUMAN	PAFAH1B2	Platelet-activating factor acetylhydrolase IB subunit beta (Fra	0.9488	5.14	1	1	1
						IIVLGLLPR	2	0.9488	1
Q5402-1	J3KP07	J3KP07_HUMAN	GAS6	Growth arrest-specific protein 6	1.0000	25.52	14	15	27
Q5402-2	Q14393	GAS6_HUMAN	GAS6	Growth arrest-specific protein 6	1.0000	25.52	14	15	27
Q5402-3	Q14393-2	GAS6_HUMAN	GAS6	Isoform 2 of Growth arrest-specific protein 6	1.0000	27.14	14	15	27
Q5402-4	Q14393-3	GAS6_HUMAN	GAS6	Isoform 3 of Growth arrest-specific protein 6	1.0000	29.49	14	15	27
						AGGLPDPVPTSAFVYR	2	0.9212	1
						DGEATLEVDGTR	2	0.9992	3
						DLVQPINPR	2	0.9996	1
						DVDECLQGR	2	0.9996	1
						GGSEVSAAQLQER	2	0.9997	1
						GSFYPGSGFAFYSLDMR	2	0.9997	3
						HSDIHAGSCPPEVPA	2	0.9852	1
						IYAVAGDLFQPER	2	0.9997	2
						LLDLDEAAYK	2	0.996	2
						MQCFSVTER	2	0.9756	1
						QLVVLAVETALALMEIK	3	0.9991	2
						SPVLTFAAGGLPDPVPTSAFVYR	2	0.999	2
						SPVLTFAAGGLPDPVPTSAFVYR	3	0.9978	2
						TCQDIDEGADSEACGEAR	2	0.9997	3
						VCDGGEHVTVLSLR	2	0.9898	2
Q5403-1	J3KPC0	J3KPC0_HUMAN	ZFAND4	AN1-type zinc finger protein 4	0.9880	4.44	2	2	2
Q5403-2	Q5VVY6	Q5VVY6_HUMAN	ZFAND4	AN1-type zinc finger protein 4	0.9880	4.76	2	2	2
Q5403-3	Q86XD8	ZFAN4_HUMAN	ZFAND4	AN1-type zinc finger protein 4	0.9880	3.99	2	2	2
						DITEMTNK	2	0.9002	1
						LQPSSQSOLDVNITDSSFSR	2	0.8796	1
Q5404-1	J3KQ32	J3KQ32_HUMAN	OLA1	Obg-like ATPase 1	1.0000	6.73	2	3	5
Q5404-2	Q9NTK5	OLA1_HUMAN	OLA1	Obg-like ATPase 1	1.0000	7.07	2	3	5
						IPAFNLVVDIAGLVK	2	0.9997	3
						IPAFNLVVDIAGLVK	3	0.9488	1
						NYVEDGDIIFFK	2	0.9898	1
Q5405-1	J3KR24	J3KR24_HUMAN	IARS	Isoleucine-tRNA ligase, cytoplasmic	1.0000	1.56	2	2	2
						VCMDFNIR	2	0.992	1
						YHIEELNVR	2	0.9564	1
Q5406-1	J3Q5F0	J3Q5F0_HUMAN	PSMC5	26S protease regulatory subunit 8	1.0000	18.93	2	2	4
Q5406-2	J3KR22	J3KR22_HUMAN	PSMC5	26S protease regulatory subunit 8 (Fragment)	1.0000	13.28	2	2	4
Q5406-3	J3QLH6	J3QLH6_HUMAN	PSMC5	26S protease regulatory subunit 8 (Fragment)	1.0000	14.88	2	2	4
Q5406-4	J3QQM1	J3QQM1_HUMAN	PSMC5	26S protease regulatory subunit 8 (Fragment)	1.0000	12.17	2	2	4
Q5406-5	J3Q5A9	J3Q5A9_HUMAN	PSMC5	26S protease regulatory subunit 8 (Fragment)	1.0000	12.45	2	2	4
						IEELQLVNDK	2	0.9964	2
						LLREELQLLQEGSYGVEVVR	3	0.9983	2
Q5407-1	Q724W1	DCXR_HUMAN	DCXR	L-xylulose reductase	0.9705	4.92	1	1	1
Q5407-2	J3KS22	J3KS22_HUMAN	DCXR	L-xylulose reductase (Fragment)	0.9705	5.38	1	1	1
Q5407-3	J3Q536	J3Q536_HUMAN	DCXR	L-xylulose reductase (Fragment)	0.9705	5.33	1	1	1
						GTVDLHATGAR	2	0.9705	1
Q5408-1	J3QQU6	J3QQU6_HUMAN	SECTM1	Secreted and transmembrane protein 1	1.0000	35.57	4	7	16
Q5408-2	Q8WVY6	SECTM1_HUMAN	SECTM1	Secreted and transmembrane protein 1	1.0000	21.37	4	7	16
Q5408-3	J3KSN0	J3KSN0_HUMAN	SECTM1	Secreted and transmembrane protein 1 (Fragment)	1.0000	36.3	4	7	16
Q5408-4	J3KTR4	J3KTR4_HUMAN	SECTM1	Secreted and transmembrane protein 1 (Fragment)	1.0000	29.78	4	7	16
Q5408-5	J3QKK2	J3QKK2_HUMAN	SECTM1	Secreted and transmembrane protein 1 (Fragment)	1.0000	31.18	4	7	16
						AHGQESAIFNEVAPGYFSR	2	0.9997	2
						AHGQESAIFNEVAPGYFSR	3	0.9996	3
						DGWQLQVQGVGAQLVIK	2	0.9994	4
						DGWQLQVQGVGAQLVIK	3	0.9992	3
						DSHAGLYMWHLVGHQR	2	0.9996	1
						DSHAGLYMWHLVGHQR	3	0.9978	2
						RAHGQESAIFNEVAPGYFSR	3	0.8699	1
Q5409-1	J3KSR8	J3KSR8_HUMAN	SRSF1	Serine/arginine-rich-splicing factor 1 (Fragment)	1.0000	15.38	2	2	4
						EAGDVCYADVIR	2	0.9997	2
						SHEGETAYIR	2	0.9996	2
Q5410-1	Q07955	SRSF1_HUMAN	SRSF1	Serine/arginine-rich splicing factor 1	1.0000	37.5	10	10	24

Q5410-2	J3KTL2	J3KTL2_HUMAN	SRSF1	Serine/arginine-rich-splicing factor 1	1.0000	36.76	10	10	24
						DGTGVVEFVR	2	0.9724	1
						EAGDVVCYADVVR	2	0.9997	2
						GGPPFAFVEFEDPR	2	0.9995	5
						GGPPFAFVEFEDPRDAEDAVYGR	3	0.9792	1
						IVGNLPPDIR	2	0.9993	9
						KEDMTYAVR	2	0.9498	1
						LVVEFPR	2	0.8397	1
						RGPPFAFVEFEDPR	3	0.9958	1
						SHEGETAYIR	2	0.9996	2
						TKDIEDVFK	2	0.9627	1
Q5411-1	J3QKT2	J3QKT2_HUMAN	CNDP2	Cytosolic non-specific dipeptidase (Fragment)	1.0000	4.02	1	1	1
Q5411-2	J3QRH4	J3QRH4_HUMAN	CNDP2	Cytosolic non-specific dipeptidase (Fragment)	1.0000	4.9	1	1	1
						TGQEIPVNVNR	2	0.9962	1
Q5412-1	P00738	HPT_HUMAN	HP	Haptoglobin	1.0000	19.7	5	5	10
Q5412-2	J3QLC9	J3QLC9_HUMAN	HP	Haptoglobin (Fragment)	1.0000	21.92	5	5	10
Q5412-3	P00738-2	HPT_HUMAN	HP	Isoform 2 of Haptoglobin	1.0000	23.05	5	5	10
						IAPTLLTYVGK	2	0.909	1
						SCAAEYGVYVK	2	0.9997	4
						TGEGQVTLNNEK	2	0.8743	1
						VTSIQDWVQK	2	0.9993	2
						YQEDCTYGDAGSAFAVHDEEDTWYATGILSFDK	3	0.9973	2
Q5413-1	J3QLP3	J3QLP3_HUMAN	VWA1	von Willebrand factor A domain-containing protein 1 (Fragment)	1.0000	31.14	3	3	3
						EQLFAEASGARGVPK	2	0.9951	1
						GNFLESAASAPAEK	2	0.9977	1
						VREFVGQLVAPLPLGTGALR	3	0.9076	1
Q5414-1	Q14974	IMB1_HUMAN	KPNB1	Importin subunit beta-1	0.9013	1.71	1	1	2
Q5414-2	J3QR48	J3QR48_HUMAN	KPNB1	Importin subunit beta-1 (Fragment)	0.9013	10.14	1	1	2
						AAVENLPTFLVELSR	2	0.9013	2
Q5415-1	J3QRR0	J3QRR0_HUMAN	VWA1	von Willebrand factor A domain-containing protein 1 (Fragment)	0.9995	13.51	2	2	2
						EFVGQLVAPLPLGTGALR	2	0.9926	1
						VREFVGQLVAPLPLGTGALR	3	0.9076	1
Q5416-1	J3QR53	J3QR53_HUMAN	MYL12A	Myosin regulatory light chain 12A	1.0000	16.95	2	2	3
Q5416-2	P19105	ML12A_HUMAN	MYL12A	Myosin regulatory light chain 12A	1.0000	17.54	2	2	3
Q5416-3	Q14950	ML12B_HUMAN	MYL12B	Myosin regulatory light chain 12B	1.0000	17.44	2	2	3
						GNNFYIEFTR	2	0.9944	2
						NAFACFDEEATGTIGEDYLR	2	0.993	1
Q5417-1	O00231	PSD11_HUMAN	PSMD11	26S proteasome non-ATPase regulatory subunit 11	0.9054	3.08	1	1	2
Q5417-2	J3QR44	J3QR44_HUMAN	PSMD11	26S proteasome non-ATPase regulatory subunit 11 (Fragment)	0.9054	6.95	1	1	2
Q5417-3	O00231-2	PSD11_HUMAN	PSMD11	Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11	0.9054	3.07	1	1	2
						EQSILEGLSLAK	2	0.9054	2
Q5418-1	J3Q5T3	J3Q5T3_HUMAN	KRT3	Keratin, type II cytoskeletal 3	1.0000	2.38	1	1	3
Q5418-2	P12035	K2C3_HUMAN	KRT3	Keratin, type II cytoskeletal 3	1.0000	2.39	1	1	3
						DVDSAYMNVKELQAK	2	0.9835	3
Q5419-1	Q05707	COE1A_HUMAN	COL14A1	Collagen alpha-1(XIV) chain	0.9788	1.39	2	2	2
Q5419-2	J3Q783	J3Q783_HUMAN	COL14A1	Collagen alpha-1(XIV) chain (Fragment)	0.9788	2.97	2	2	2
Q5419-3	Q05707-2	COE1A_HUMAN	COL14A1	Isoform 2 of Collagen alpha-1(XIV) chain	0.9788	1.4	2	2	2
Q5419-4	Q05707-3	COE1A_HUMAN	COL14A1	Isoform 3 of Collagen alpha-1(XIV) chain	0.9788	1.47	2	2	2
						NLVVGDETTSSLRV	2	0.8638	1
						QESTVGGTTR	2	0.8441	1
Q5420-1	K7EIV0	K7EIV0_HUMAN	CAPNS1	Calpain small subunit 1 (Fragment)	1.0000	15.82	2	2	3
						ILGGVISAISEAAQYNPEPPPR	3	0.9975	2
						LGFEFK	2	0.9897	1
Q5421-1	K7EJ44	K7EJ44_HUMAN	PFN1	Profilin 1, isoform CRA_b	1.0000	13.46	1	1	5
						DSLQDGEFSMDLR	2	0.9995	5
Q5422-1	K7EJ74	K7EJ74_HUMAN	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)	1.0000	6.72	1	1	1
						YDWDLAAR	2	0.9995	1
Q5423-1	K7EJ03	K7EJ03_HUMAN	LGALS3BP	Galectin-3-binding protein	1.0000	10.24	1	2	6
Q5423-2	K7EN99	K7EN99_HUMAN	LGALS3BP	Galectin-3-binding protein	1.0000	18.58	1	2	6
Q5423-3	K7ER26	K7ER26_HUMAN	LGALS3BP	Galectin-3-binding protein	1.0000	16.03	1	2	6
Q5423-4	K7ES75	K7ES75_HUMAN	LGALS3BP	Galectin-3-binding protein (Fragment)	1.0000	23.86	1	2	6
						GGWGTVCNLDLWLDASVVCRR	2	0.9997	4
						GGWGTVCNLDLWLDASVVCRR	3	0.9969	2
Q5424-1	K7EJP1	K7EJP1_HUMAN	ATP5A1	ATP synthase subunit alpha, mitochondrial (Fragment)	1.0000	21.53	2	2	5
Q5424-2	K7EK77	K7EK77_HUMAN	ATP5A1	ATP synthase subunit alpha, mitochondrial (Fragment)	1.0000	14.98	2	2	5
Q5424-3	K7EQH4	K7EQH4_HUMAN	ATP5A1	ATP synthase subunit alpha, mitochondrial (Fragment)	1.0000	27.93	2	2	5
Q5424-4	K7ERX7	K7ERX7_HUMAN	ATP5A1	ATP synthase subunit alpha, mitochondrial (Fragment)	1.0000	15.12	2	2	5
						ILGADTSVDEETGR	2	0.9997	2
						TGAIVDPVPEELLGR	2	0.9996	3
Q5425-1	K7EK57	K7EK57_HUMAN	RPL22	60S ribosomal protein L22	0.9608	24.53	1	1	1
Q5425-2	K7ER17	K7ER17_HUMAN	RPL22	60S ribosomal protein L22	0.9608	13.68	1	1	1
Q5425-3	P35268	RL22_HUMAN	RPL22	60S ribosomal protein L22	0.9608	10.16	1	1	1
Q5425-4	K7EJ75	K7EJ75_HUMAN	RPL22	60S ribosomal protein L22 (Fragment)	0.9608	27.66	1	1	1
Q5425-5	K7ELC4	K7ELC4_HUMAN	RPL22	60S ribosomal protein L22 (Fragment)	0.9608	16.46	1	1	1
Q5425-6	K7EMH1	K7EMH1_HUMAN	RPL22	60S ribosomal protein L22 (Fragment)	0.9608	14.61	1	1	1
Q5425-7	K7EP65	K7EP65_HUMAN	RPL22	60S ribosomal protein L22 (Fragment)	0.9608	27.08	1	1	1
Q5426-1	K7EKD8	K7EKD8_HUMAN	CAPNS1	Calpain small subunit 1	0.9889	21.43	1	1	1
Q5426-2	K7ES78	K7ES78_HUMAN	CAPNS1	Calpain small subunit 1 (Fragment)	0.9889	70.83	1	1	1
						GGGGGGGGGGGLGGGLGNVLGGLSGAGGGGGGGGGGGGGGGGGGTAMR	4	0.9478	1
Q5427-1	Q92692-2	PVRL2_HUMAN	PVRL2	Isoform Alpha of Nectin-2	0.9607	2.51	1	1	2
Q5427-2	Q92692	PVRL2_HUMAN	PVRL2	Nectin-2	0.9607	2.23	1	1	2
Q5427-3	K7KE8	K7KE8_HUMAN	PVRL2	Nectin-2 (Fragment)	0.9607	5.71	1	1	2
						ISWLSLDWEAK	2	0.9607	2
Q5428-1	K7KF6	K7KF6_HUMAN	ANGPTL6	Angiopoietin-related protein 6	1.0000	6.05	2	2	2
Q5428-2	Q8NI99	ANGL6_HUMAN	ANGPTL6	Angiopoietin-related protein 6	1.0000	5.53	2	2	2
						GDHELLVLEDWGGR	3	0.9691	1
						YQDGVVWAEFR	2	0.9353	1
Q5429-1	K7EK18	K7EK18_HUMAN	PPL	Periplakin	1.0000	2.05	3	3	4
Q5429-2	O60437	PEPL_HUMAN	PPL	Periplakin	1.0000	2.05	3	3	4
						LQNLLEFALLLR	2	0.9996	2
						NQLQLELEALQLQLR	3	0.9966	1
						YQIELLLR	2	0.9946	1
Q5430-1	P26599-2	PTBP1_HUMAN	PTBP1	Isoform 2 of Polypyrimidine tract-binding protein 1	0.9995	5.09	2	2	3
Q5430-2	P26599-3	PTBP1_HUMAN	PTBP1	Isoform 3 of Polypyrimidine tract-binding protein 1	0.9995	5.03	2	2	3
Q5430-3	P26599	PTBP1_HUMAN	PTBP1	Polypyrimidine tract-binding protein 1	0.9995	5.27	2	2	3
Q5430-4	K7EKJ7	K7EKJ7_HUMAN	PTBP1	Polypyrimidine tract-binding protein 1 (Fragment)	0.9995	11.86	2	2	3
Q5430-5	K7ELW5	K7ELW5_HUMAN	PTBP1	Polypyrimidine tract-binding protein 1 (Fragment)	0.9995	12.02	2	2	3
Q5430-6	K7ES59	K7ES59_HUMAN	PTBP1	Polypyrimidine tract-binding protein 1 (Fragment)	0.9995	11.07	2	2	3
						KLPIDVTEGEVISLGLPFGK	3	0.9876	2
						VTNIMLMLK	2	0.9582	1
Q5431-1	K7EKQ5	K7EKQ5_HUMAN	LGALS3BP	Galectin-3-binding protein	1.0000	16.67	2	3	8
Q5431-2	K7EP36	K7EP36_HUMAN	LGALS3BP	Galectin-3-binding protein (Fragment)	1.0000	13.51	2	3	8
Q5431-3	K7ESM3	K7ESM3_HUMAN	LGALS3BP	Galectin-3-binding protein (Fragment)	1.0000	16.75	2	3	8
						ELSEALGOIFDSQR	2	0.999	2
						GGWGTVCNLDLWLDASVVCRR	2	0.9997	4
						GGWGTVCNLDLWLDASVVCRR	3	0.9969	2
Q5432-1	K7EL21	K7EL21_HUMAN	CAPS	Calcyphosin	1.0000	26.18	7	7	11
Q5432-2	Q13938	CATP1_HUMAN	CAPS	Calcyphosin	1.0000	38.1	7	7	11
						ALRPPMSQAR	2	0.9782	1
						EAVIAAFAK	2	0.9987	1
						LGLVLDQAEAGVCR	2	0.9997	2
						NGSGTLDLEEFRL	2	0.9993	3
						SGDGVTVVDLRL	2	0.9981	1
						SGEWTEDEVLR	2	0.9977	2
						SGEWTEDEVLR	2	0.9021	1
Q5433-1	K7ELJ7	K7ELJ7_HUMAN	CAPNS1	Calpain small subunit 1	1.0000	29.5	3	3	4
Q5433-2	P04632	CPNS1_HUMAN	CAPNS1	Calpain small subunit 1	1.0000	30.6	3	3	4
						GGGGGGGGGGGLGGGLGNVLGGLSGAGGGGGGGGGGGGGGGGGGTAMR	4	0.9478	1
						ILGGVISAISEAAQYNPEPPPR	3	0.9975	2
						LGFEFK	2	0.9897	1
Q5434-1	K7ELI7	K7ELI7_HUMAN	PRKCSH	Glucosidase 2 subunit beta	1.0000	4.11	2	2	2
Q5434-2	P14314	GLU2B_HUMAN	PRKCSH	Glucosidase 2 subunit beta	1.0000	4.17	2	2	2

Q5434-3	P14314-2	GLU2B_HUMAN	PRKCSH	Isoform 2 of Glucosidase 2 subunit beta	1.0000	4.19	2	2	2
						ETMVTSTTEPSR	2	0.9994	1
						SKDMEESIR	2	0.9091	1
Q5435-1	K7EM20	K7EM20_HUMAN	YWHAE	14-3-3 protein epsilon (Fragment)	1.0000	11.3	1	1	2
						SVFYIELNSPDR	2	0.9476	2
Q5436-1	K7EM49	K7EM49_HUMAN	PGD	6-phosphogluconate dehydrogenase, decarboxylating (Fragment)	1.0000	8.29	1	1	2
Q5436-2	K7EMN2	K7EMN2_HUMAN	PGD	6-phosphogluconate dehydrogenase, decarboxylating (Fragment)	1.0000	10.63	1	1	2
Q5436-3	K7EPF6	K7EPF6_HUMAN	PGD	6-phosphogluconate dehydrogenase, decarboxylating (Fragment)	1.0000	6.64	1	1	2
						GILFVSGVSGGEEGAR	2	0.9993	2
Q5437-1	K7EM73	K7EM73_HUMAN	CAPNS1	Calpain small subunit 1 (Fragment)	1.0000	46.01	2	2	3
						GGGGGGGGGGLGGGLGNVLGGISGAGGGGGGGGGGGGGGGGTAMR	4	0.9478	1
						ILGGVISIAEAAQYNPEPPPR	3	0.9975	2
Q5438-1	P26368-2	U2AF2_HUMAN	U2AF2	Isoform 2 of Splicing factor U2AF 65 kDa subunit	1.0000	15.71	5	5	6
Q5438-2	K7ENG2	K7ENG2_HUMAN	U2AF2	Splicing factor U2AF 65 kDa subunit	1.0000	24.1	5	5	6
Q5438-3	P26368	U2AF2_HUMAN	U2AF2	Splicing factor U2AF 65 kDa subunit	1.0000	15.58	5	5	6
						ELLTSFGLPK	2	0.9874	1
						IFVEFTSVFDCQK	2	0.9195	1
						LGGLTOAPGNPLVAVQIQDNFALFELR	3	0.9908	2
						NFAFLFR	2	0.9898	1
						SVDETQAMAFQGIHFQGSCLK	2	0.9988	1
Q5439-1	Q15029	U5S1_HUMAN	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	1.0000	2.67	2	2	2
Q5439-2	K7EP67	K7EP67_HUMAN	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component (Fragment)	1.0000	11.66	2	2	2
Q5439-3	Q15029-2	U5S1_HUMAN	EFTUD2	Isoform 2 of 116 kDa U5 small nuclear ribonucleoprotein component	1.0000	2.77	2	2	2
Q5439-4	Q15029-3	U5S1_HUMAN	EFTUD2	Isoform 3 of 116 kDa U5 small nuclear ribonucleoprotein component	1.0000	2.7	2	2	2
						GLAEDIENEVQITWNR	2	0.9986	1
						YDWDLAAR	2	0.9995	1
Q5440-1	K7EQ48	K7EQ48_HUMAN	GPI	Glucose-6-phosphate isomerase	1.0000	15.61	6	8	16
Q5440-2	P06744	G6PI_HUMAN	GPI	Glucose-6-phosphate isomerase	1.0000	13.26	6	8	16
Q5440-3	P06744-2	G6PI_HUMAN	GPI	Isoform 2 of Glucose-6-phosphate isomerase	1.0000	13.01	6	8	16
						HFVALSTNTTK	2	0.9986	2
						NLVTEVDMR	2	0.9912	1
						TFTTQETITNAETAK	2	0.9997	2
						TFTTQETITNAETAKFWLQAAK	3	0.8798	1
						TLAQLNPESSLFIASK	2	0.9997	3
						TLAQLNPESSLFIASK	3	0.9991	3
						VWYVSNIDGTHIAK	2	0.9985	2
						VWYVSNIDGTHIAK	3	0.9942	2
Q5441-1	K7EQ71	K7EQ71_HUMAN	PPL	Periplakin (Fragment)	1.0000	2.51	2	2	3
						LQNLFEALNLLR	2	0.9996	2
						NQLLQEELEALQLRL	3	0.9966	1
Q5442-1	P13646-3	K1C13_HUMAN	KRT13	Isoform 3 of Keratin, type I cytoskeletal 13	1.0000	47.14	16	18	32
Q5442-2	K7ERE3	K7ERE3_HUMAN	KRT13	Keratin, type I cytoskeletal 13	1.0000	47.71	16	18	32
Q5442-3	P13646	K1C13_HUMAN	KRT13	Keratin, type I cytoskeletal 13	1.0000	43.23	16	18	32
						AGLETVATEECR	2	0.9991	2
						ALEEANADLSVK	2	0.9994	2
						EVSTNTAMIQTSK	2	0.9956	1
						LASYLEK	2	0.974	1
						LKYENELALR	2	0.9829	1
						LKYENELALR	3	0.9904	1
						LQSSASVSGGGGGGSCQLGGGR	2	0.9997	2
						LTMQNLNDR	2	0.98	1
						QSVADINGLRR	2	0.9455	1
						SEMCEQNGEYK	2	0.9989	2
						SLLEGQDAK	2	0.9793	1
						TDLEMQIESLNEELAYMK	2	0.9988	1
						TIEELNOK	2	0.9766	1
						TLQGLEIELQSLSMK	2	0.9997	2
						TLQGLEIELQSLSMK	3	0.9996	4
						VILEIDNAR	2	0.998	4
						VDELITLSK	2	0.9989	2
						YALQLQIQIGLISSIEAQLSELR	3	0.9996	3
Q5443-1	P55083-2	MFAP4_HUMAN	MFAP4	Isoform 2 of Microfibril-associated glycoprotein 4	1.0000	15.77	2	2	7
Q5443-2	K7ES70	K7ES70_HUMAN	MFAP4	Microfibril-associated glycoprotein 4	1.0000	15.71	2	2	7
Q5443-3	P55083	MFAP4_HUMAN	MFAP4	Microfibril-associated glycoprotein 4	1.0000	17.25	2	2	7
						ADGEYWLGLQNMHLLTK	3	0.9994	5
						FSTFDRDQDLFVQCAALSSGAFWFR	3	0.9974	2
Q5444-1	K7ESA0	K7ESA0_HUMAN	ATPSA1	ATP synthase subunit alpha, mitochondrial	1.0000	19.48	1	1	2
Q5444-2	P25705-3	ATPA_HUMAN	ATPSA1	Isoform 3 of ATP synthase subunit alpha, mitochondrial	1.0000	2.82	1	1	2
						ILGADTSVDELTEGR	2	0.9997	2
Q5445-1	MOQX47	MOQX47_HUMAN	GMFG	Glia maturation factor gamma	0.9610	17.61	1	1	4
Q5445-2	MOQY68	MOQY68_HUMAN	GMFG	Glia maturation factor gamma	0.9610	13.98	1	1	4
Q5445-3	MOR0C1	MOR0C1_HUMAN	GMFG	Glia maturation factor gamma	0.9610	11.93	1	1	4
Q5445-4	MOR1D2	MOR1D2_HUMAN	GMFG	Glia maturation factor gamma	0.9610	12.87	1	1	4
Q5445-5	O60234	GMFG_HUMAN	GMFG	Glia maturation factor gamma	0.9610	9.15	1	1	4
						TTDDLTEAWLQEK	2	0.961	4
Q5446-1	MOQYT0	MOQYT0_HUMAN		Uncharacterized protein (Fragment)	0.9794	4.05	1	1	3
Q5446-2	MOR076	MOR076_HUMAN		Uncharacterized protein (Fragment)	0.9794	11.4	1	1	3
Q5446-3	P14866	HNRPL_HUMAN	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	0.9794	2.21	1	1	3
Q5446-4	MOQX55	MOQX55_HUMAN	HNRNPL	Heterogeneous nuclear ribonucleoprotein L (Fragment)	0.9794	2.45	1	1	3
Q5446-5	P14866-2	HNRPL_HUMAN	HNRNPL	Isoform 2 of Heterogeneous nuclear ribonucleoprotein L	0.9794	2.85	1	1	3
						VFNVFLCYGNVEK	2	0.9794	3
Q5447-1	Q13985	Q13985_HUMAN	CEA	Carcinoembryonic antigen	1.0000	19.4	1	1	2
						EVLLLAHLPLQNR	2	0.9993	2
Q5448-1	MOQZL1	MOQZL1_HUMAN	BLVRB	Flavin reductase (NADPH)	1.0000	9.74	1	1	3
Q5448-2	MOR192	MOR192_HUMAN	BLVRB	Flavin reductase (NADPH)	1.0000	9.2	1	1	3
						TVAGQDAVIVLLGTR	2	0.9996	3
Q5449-1	MOQZN2	MOQZN2_HUMAN	RP55	40S ribosomal protein S5	0.9719	11.19	1	1	3
Q5449-2	MOR0R2	MOR0R2_HUMAN	RP55	40S ribosomal protein S5	0.9719	6.67	1	1	3
Q5449-3	P46782	RS5_HUMAN	RP55	40S ribosomal protein S5	0.9719	7.35	1	1	3
Q5449-4	MOR0F0	MOR0F0_HUMAN	RP55	40S ribosomal protein S5 (Fragment)	0.9719	7.5	1	1	3
						TIAELADELINAAK	2	0.9719	3
Q5450-1	P52272	HNRPM_HUMAN	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	0.9575	2.19	1	1	1
Q5450-2	MOR019	MOR019_HUMAN	HNRNPM	Heterogeneous nuclear ribonucleoprotein M (Fragment)	0.9575	4.55	1	1	1
Q5450-3	MOR0N3	MOR0N3_HUMAN	HNRNPM	Heterogeneous nuclear ribonucleoprotein M (Fragment)	0.9575	5.82	1	1	1
Q5450-4	MOR270	MOR270_HUMAN	HNRNPM	Heterogeneous nuclear ribonucleoprotein M (Fragment)	0.9575	4.48	1	1	1
Q5450-5	P52272-2	HNRPM_HUMAN	HNRNPM	Isoform 2 of Heterogeneous nuclear ribonucleoprotein M	0.9575	2.32	1	1	1
						VGEYTYVELMDAEGK	2	0.9575	1
Q5451-1	MOR0U3	MOR0U3_HUMAN	PGLS	6-phosphogluconolactonase	1.0000	18.99	3	3	8
						AACCLAGAR	2	0.999	1
						ELPAAVAPAGPASLAR	2	0.9994	4
						WTLGFCDER	2	0.9992	3
Q5452-1	MOR0Y2	MOR0Y2_HUMAN	NAPA	Alpha-soluble NSF attachment protein	1.0000	10.94	2	2	4
Q5452-2	P54920	SNA4_HUMAN	NAPA	Alpha-soluble NSF attachment protein	1.0000	9.49	2	2	4
Q5452-3	MOR2M1	MOR2M1_HUMAN	NAPA	Alpha-soluble NSF attachment protein (Fragment)	1.0000	10.45	2	2	4
						NSQSFPSGLFGSSK	2	0.9996	2
						VAGYALLLEQYK	2	0.9996	2
Q5453-1	O95336	6PGL_HUMAN	PGLS	6-phosphogluconolactonase	1.0000	22.09	5	5	11
Q5453-2	MOR261	MOR261_HUMAN	PGLS	6-phosphogluconolactonase (Fragment)	1.0000	26.39	5	5	11
						AACCLAGAR	2	0.999	1
						ELPAAVAPAGPASLAR	2	0.9994	4
						TVIFVATGEGK	2	0.9857	1
						VTLTPLVLNAR	2	0.9937	2
						WTLGFCDER	2	0.9992	3
Q5454-1	Q15102	PA1B3_HUMAN	PAFAH1B3	Platelet-activating factor acetylhydrolase IB subunit gamma	0.9436	3.9	1	1	1
Q5454-2	MOR389	MOR389_HUMAN	PAFAH1B3	Platelet-activating factor acetylhydrolase IB subunit gamma	0.9436	5.49	1	1	1
						VVLGLLPR	2	0.9436	1
Q5455-1	Q8IV08	PLD3_HUMAN	PLD3	Phospholipase D3	0.9669	1.84	1	1	1
Q5455-2	MOR3G9	MOR3G9_HUMAN	PLD3	Phospholipase D3 (Fragment)	0.9669	12.68	1	1	1
						SQLEAFILR	2	0.9669	1
Q5456-1	O00187	MASFP2_HUMAN	MASFP2	Mannan-binding lectin serine protease 2	1.0000	16.33	48	58	235
						APGKDTFYSYGSSLDITFR	2	0.9283	1
						APGKDTFYSYGSSLDITFR	2	0.9997	8
						APGKDTFYSYGSSLDITFR	3	0.9995	41

						ATLCGQESTDTER	2	0.9978	7
						ATLCGQESTDTERAPGK	2	0.9712	2
						ATLCGQESTDTERAPGKDTFYSLGSSLDITFR	3	0.8687	1
						DLESHLCEYDFVK	2	0.9959	3
						DTFYSLGSSLDITFR	2	0.9997	37
						DTFYSLGSSLDITFR	3	0.9994	4
						FYSLGSSLDITFR	2	0.9726	2
						GKDTFYSLGSSLDITFR	2	0.9888	4
						GKDTFYSLGSSLDITFR	3	0.9618	2
						KDTFYSLGSSLDITFR	3	0.8956	1
						LASPGFPGEYANDQERR	2	0.9997	7
						LASPGFPGEYANDQERR	2	0.999	6
						LASPGFPGEYANDQERR	3	0.9826	1
						LATLCGQESTDTER	2	0.9907	3
						LGSSLDITFR	2	0.9945	2
						LSHLCEYDFVK	2	0.8737	1
						LYFTHFDELSHL	2	0.8293	1
						LYFTHFDELSHL	3	0.8909	1
						LYFTHFDELSHLCE	2	0.9704	2
						LYFTHFDELSHLCEY	2	0.8552	1
						LYFTHFDELSHLCEYDF	2	0.8348	1
						LYFTHFDELSHLCEYDFV	2	0.9796	1
						LYFTHFDELSHLCEYDFVK	2	0.9997	1
						LYFTHFDELSHLCEYDFVK	3	0.9997	12
						LYFTHFDELSHLCEYDFVK	4	0.9989	7
						RLYFTHFDELSHLCEYDFVK	3	0.9001	2
						RLYFTHFDELSHLCEYDFVK	4	0.9247	1
						RWTLTAPPGYR	3	0.9445	1
						SDYSNEKPF	2	0.9809	1
						SDYSNEKPFT	2	0.9584	1
						SDYSNEKPFTG	2	0.9984	2
						SDYSNEKPFTGF	2	0.9982	3
						SDYSNEKPFTGFE	2	0.9957	3
						SDYSNEKPFTGFEA	2	0.9978	3
						SDYSNEKPFTGFEAF	2	0.9985	4
						SDYSNEKPFTGFEAFY	2	0.9927	3
						SDYSNEKPFTGFEAFYA	2	0.936	1
						SDYSNEKPFTGFEAFYAAEDID	2	0.9466	1
						SLGSSLDITFR	2	0.9986	2
						TFYSLGSSLDITFR	2	0.9988	8
						THFDELSHLCEYDFVK	2	0.9847	1
						THFDELSHLCEYDFVK	3	0.9049	1
						TLGCGQESTDTER	2	0.9928	5
						TLGCGQESTDTERAPGK	2	0.8024	1
						VLATLCGQESTDTER	2	0.9997	7
						VLATLCGQESTDTERA	2	0.9769	1
						VLATLCGQESTDTERAPG	2	0.9852	4
						VLATLCGQESTDTERAPGK	2	0.9996	2
						VLATLCGQESTDTERAPGK	3	0.9991	3
						VLATLCGQESTDTERAPGKD	2	0.9807	1
						VLATLCGQESTDTERAPGKDT	2	0.9779	1
						VLATLCGQESTDTERAPGKDTFYSLGSSLDITFR	3	0.9993	4
						WPEPVFGR	2	0.9995	3
						WTLTAPPGYR	2	0.9997	4
						YSLGSSLDITFR	2	0.9925	1
Q5457-1	O00187-2	MASP2_HUMAN	MASP2	Isoform 2 of Mannan-binding lectin serine protease 2	1.0000	60.54	48	57	234
						APGKDTFYSLGSSLDITFR	2	0.9983	1
						APGKDTFYSLGSSLDITFR	2	0.9997	8
						APGKDTFYSLGSSLDITFR	3	0.9995	41
						ATLCGQESTDTER	2	0.9978	7
						ATLCGQESTDTERAPGK	2	0.9712	2
						ATLCGQESTDTERAPGKDTFYSLGSSLDITFR	3	0.8687	1
						DLESHLCEYDFVK	2	0.9959	3
						DTFYSLGSSLDITFR	2	0.9997	37
						DTFYSLGSSLDITFR	3	0.9994	4
						FYSLGSSLDITFR	2	0.9726	2
						GKDTFYSLGSSLDITFR	2	0.9888	4
						GKDTFYSLGSSLDITFR	3	0.9618	2
						KDTFYSLGSSLDITFR	3	0.8956	1
						LASPGFPGEYANDQERR	2	0.9997	7
						LASPGFPGEYANDQERR	2	0.999	6
						LASPGFPGEYANDQERR	3	0.9826	1
						LATLCGQESTDTER	2	0.9907	3
						LGSSLDITFR	2	0.9945	2
						LSHLCEYDFVK	2	0.8737	1
						LYFTHFDELSHL	2	0.8293	1
						LYFTHFDELSHL	3	0.8909	1
						LYFTHFDELSHLCE	2	0.9704	2
						LYFTHFDELSHLCEY	2	0.8552	1
						LYFTHFDELSHLCEYDF	2	0.8348	1
						LYFTHFDELSHLCEYDFV	2	0.9796	1
						LYFTHFDELSHLCEYDFVK	2	0.9997	1
						LYFTHFDELSHLCEYDFVK	3	0.9997	12
						LYFTHFDELSHLCEYDFVK	4	0.9989	7
						RLYFTHFDELSHLCEYDFVK	3	0.9001	2
						RLYFTHFDELSHLCEYDFVK	4	0.9247	1
						RWTLTAPPGYR	3	0.9445	1
						SDYSNEKPF	2	0.9809	1
						SDYSNEKPFT	2	0.9584	1
						SDYSNEKPFTG	2	0.9984	2
						SDYSNEKPFTGF	2	0.9982	3
						SDYSNEKPFTGFE	2	0.9957	3
						SDYSNEKPFTGFEA	2	0.9978	3
						SDYSNEKPFTGFEAF	2	0.9985	4
						SDYSNEKPFTGFEAFY	2	0.9927	3
						SDYSNEKPFTGFEAFYA	2	0.936	1
						SDYSNEKPFTGFEAFYAAEDID	2	0.9466	1
						SLGSSLDITFR	2	0.9986	2
						TFYSLGSSLDITFR	2	0.9988	8
						THFDELSHLCEYDFVK	2	0.9847	1
						TLGCGQESTDTER	2	0.9928	5
						TLGCGQESTDTERAPGK	2	0.8024	1
						VLATLCGQESTDTER	2	0.9997	7
						VLATLCGQESTDTERA	2	0.9769	1
						VLATLCGQESTDTERAPG	2	0.9852	4
						VLATLCGQESTDTERAPGK	2	0.9996	2
						VLATLCGQESTDTERAPGK	3	0.9991	3
						VLATLCGQESTDTERAPGKD	2	0.9807	1
						VLATLCGQESTDTERAPGKDT	2	0.9779	1
						VLATLCGQESTDTERAPGKDTFYSLGSSLDITFR	3	0.9993	4
						WPEPVFGR	2	0.9995	3
						WTLTAPPGYR	2	0.9997	4
						YSLGSSLDITFR	2	0.9925	1
Q5458-1	O00203	AP3B1_HUMAN	AP3B1	AP-3 complex subunit beta-1	1.0000	2.01	2	2	3
Q5458-2	O00203-3	AP3B1_HUMAN	AP3B1	Isoform 2 of AP-3 complex subunit beta-1	1.0000	2.11	2	2	3
						EGSTAQUINTEK	2	0.9988	2
						TVIGSVLLR	2	0.9964	1
Q5459-1	O00232	PSD12_HUMAN	PSMD12	26S proteasome non-ATPase regulatory subunit 12	1.0000	7.02	3	3	6
						ILVAVVK	2	0.9521	1
						LQEVETLSLSEK	2	0.9996	3
						MEVDYSATVDQR	2	0.9996	2
Q5460-1	O00299	CLIC1_HUMAN	CLIC1	Chloride intracellular channel protein 1	1.0000	7.05	2	2	3
						GFTIPEAFR	2	0.9935	1

Q5461-1	O00429-7	DNM1L_HUMAN	DNM1L	Isoform 7 of Dynamin-1-like protein	0.9996	LFMVLWLK	2	0.9929	2
						6.19	3	3	3
						ALQGASQIAEIR	2	0.9843	1
						KMTLLHGK	2	0.976	1
						YIETSELGGAR	2	0.9722	1
Q5462-1	O00468-2	AGRIN_HUMAN	AGRIN	Isoform 2 of Agrin	1.0000	1.02	2	2	3
						FGALCEAETGR	2	0.9995	2
						SFLAFTLR	2	0.9986	1
Q5463-1	O00468	AGRIN_HUMAN	AGRIN	Agrin	1.0000	26.8	38	41	77
Q5463-2	O00468-3	AGRIN_HUMAN	AGRIN	Isoform 3 of Agrin	1.0000	27.04	38	41	77
Q5463-3	O00468-4	AGRIN_HUMAN	AGRIN	Isoform 4 of Agrin	1.0000	26.91	38	41	77
Q5463-4	O00468-5	AGRIN_HUMAN	AGRIN	Isoform 5 of Agrin	1.0000	26.93	38	41	77
Q5463-5	O00468-6	AGRIN_HUMAN	AGRIN	Isoform 6 of Agrin	1.0000	27.09	38	41	77
Q5463-6	O00468-7	AGRIN_HUMAN	AGRIN	Isoform 7 of Agrin	1.0000	26.85	38	41	77
						AAAVSSGFDGAIQLVSLGGR	2	0.9926	1
						ALGPAGCEADASAPATCAEMR	2	0.9997	4
						ALQSNHFELSLR	2	0.9962	1
						ASCYNALGCCSDGKTPSLDAEGSNCPATK	3	0.9908	1
						AYGTGIVGCLR	2	0.998	1
						CDKCEPGFWNFR	3	0.999	2
						CEHPPPGPVCGSDGVYGSACELR	3	0.9997	4
						CEPGFWNFR	2	0.9542	1
						EAACLQQTQIEFAR	2	0.9997	1
						EEEANVLTGTVEELNVDPVQHTYSCK	3	0.9643	1
						ESLLDGGNKVISGFDPLICDNQVSTGOTR	3	0.999	3
						FDTSGSPAVLTSVAVPEPGQWHR	3	0.9873	2
						FGALCEAETGR	2	0.9995	2
						FHCQCPGR	2	0.9805	2
						FNAVCLSR	2	0.998	1
						GAPEGTVCSDGADYVPGECOLLR	2	0.9997	3
						GAPEGTVCSDGADYVPGECOLLR	3	0.9939	2
						GKDFALALDGR	3	0.9928	1
						GLHTFAR	2	0.9872	1
						GMLCGFGAVCEPMAEGPGR	2	0.9997	3
						HQGPCDQAPSPCLGVQCAFATCAVK	3	0.9479	1
						IFFVNPAPPYLPWAHK	3	0.9974	3
						KFDGPCDCQCALPDPSPR	2	0.9996	2
						KFDGPCDCQCALPDPSPR	3	0.9828	2
						KSPCPVAVPVCGSDASTYSNECELQR	3	0.9996	3
						LELIGPGAATR	2	0.9993	1
						LLOVNNQR	2	0.9981	1
						MALEVFLAR	2	0.9997	2
						QAPVCGDDGVTYENDOCVMGR	2	0.9997	2
						REEEANVLTGTVEELNVDPVQHTYSCK	3	0.997	1
						REEEANVLTGTVEELNVDPVQHTYSCK	4	0.9334	1
						SADGLTASCLCPATER	2	0.9996	2
						SFLAFTLR	2	0.9986	1
						SIESTLDDLFR	2	0.9997	2
						SPCPVAVPVCGSDASTYSNECELQR	3	0.9991	3
						SPCQPNPCHGAAPCR	2	0.9996	1
						TFVGAGLR	2	0.9946	1
						VCSDGVTYGNECOLK	2	0.9997	3
						VGPTCADEKSPCQPNPCHGAAPCR	3	0.9993	4
						VTCDGAYRPVCAQDGR	2	0.9974	2
						VVISGFDPLICDNQVSTGOTR	2	0.9997	2
Q5464-1	O00526	UPK2_HUMAN	UPK2	Uroplakin-2	0.9596	7.61	1	1	2
						LSAQVNTNVPVGTK	2	0.9596	2
Q5465-1	O00571	DDX3X_HUMAN	DDX3X	ATP-dependent RNA helicase DDX3X	1.0000	13.44	8	8	11
Q5465-2	O00571-2	DDX3X_HUMAN	DDX3X	Isoform 2 of ATP-dependent RNA helicase DDX3X	1.0000	13.78	8	8	11
						DLDDLVEAK	2	0.9988	1
						DLMACAQTSQSGK	2	0.9479	1
						ELAVQIYEER	2	0.9988	2
						GCHLLVATPGR	2	0.999	1
						HAIPK	2	0.9983	1
						HVINFDLPDIEEVVHR	3	0.8247	1
						SFLDLLNATGK	2	0.9996	3
						YVLDEADR	2	0.965	1
Q5466-1	O14556	G3PT_HUMAN	GAPDHS	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific	1.0000	4.41	2	2	3
						AGIALNDNFVK	2	0.9968	2
Q5467-1	O14773-2	TPP1_HUMAN	TPP1	Isoform 2 of Tripeptidyl-peptidase 1	1.0000	LTGMAFR	2	0.9971	1
Q5467-2	O14773	TPP1_HUMAN	TPP1	Tripeptidyl-peptidase 1	1.0000	58.75	19	22	51
						33.39	19	22	51
						ASGDSGAGCWSVSGR	2	0.9659	1
						AYPDVAALSDGYWVVSNR	2	0.9997	6
						AYPDVAALSDGYWVVSNR	3	0.9991	2
						AYPDVAALSDGYWVVSNRPIPVWVSGTSASTPVFGGILSLNEHR	4	0.9741	1
						FASGDSGAGCWSVSGR	2	0.9942	2
						FGGILSLNEHR	3	0.9551	2
						FGGNFAHQASVAR	2	0.8323	1
						GDDDESLSSAYIQR	2	0.8765	1
						GLTLFASGDSGAGCWSVSGR	2	0.9997	7
						GLTLFASGDSGAGCWSVSGR	3	0.9252	1
						HQFRPTFA	2	0.8441	1
						HQFRPTFPASSPY	2	0.8794	1
						HQFRPTFPASSPYVT	2	0.8469	1
						HQFRPTFPASSPYVTVTGTSFQEPFLITNEIV	3	0.9398	1
						ILSGRPPLGLFNPR	2	0.9992	5
						ILSGRPPLGLFNPR	3	0.9994	3
						LFNGNFAHQASVAR	2	0.9997	3
						LITNEIVDYSGGGFSNVFRPPSYQEEAVTK	3	0.8827	2
						LYQQHGAGLFDVTR	3	0.9996	3
						SYGODEDSLSSAYIQR	2	0.9871	1
						VNTELMK	2	0.9827	1
						VPIPVWVSGTSASTPVFGGILSLNEHR	3	0.9997	5
Q5468-1	O14980	XPO1_HUMAN	XPO1	Exportin-1	0.9990	3.45	2	2	2
						EFAGEDTSDFLEER	2	0.9904	1
						LDINLLDNVNVNCLYHGEAQQR	3	0.8917	1
Q5469-1	O15269	SPTCL1_HUMAN	SPTCL1	Serine palmitoyltransferase 1	0.9765	2.96	1	1	2
						VVVTEQTEELER	2	0.9765	2
Q5470-1	O43143	DHX15_HUMAN	DHX15	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase	1.0000	3.02	2	2	2
						TLATDILMGVLK	2	0.9986	1
						YGVILDEAHER	2	0.9893	1
Q5471-1	O43175	SERA_HUMAN	PHGDH	D-3-phosphoglycerate dehydrogenase	1.0000	10.88	4	4	6
						AGTGVDNVLEAATR	2	0.9994	2
						GGIVDEGALLR	2	0.999	1
						ONISKEELAEIQDCEGLIVR	3	0.9443	1
						VTADIVMAEK	2	0.9972	2
Q5472-1	O43653	PSCA_HUMAN	PSCA	Prostate stem cell antigen	1.0000	27.64	3	3	5
						AVGLLTVISK	2	0.9998	3
						GCSLNCVDDSDQYVYVK	2	0.9995	1
						LLCYSCK	2	0.9548	1
Q5473-1	O43707	ACTN4_HUMAN	ACTN4	Alpha-actinin-4	1.0000	5.49	4	4	10
Q5473-2	O43707-2	ACTN4_HUMAN	ACTN4	Isoform ACTN4I50 of Alpha-actinin-4	1.0000	7.23	4	4	10
						ETTDTDADQVIAFK	2	0.9991	2
						LASDLLEWIR	2	0.9974	3
						TINEVENQLTR	2	0.999	2
						VGWELQLTIAR	2	0.9996	3
Q5474-1	Q14533	KRT81_HUMAN	KRT81	Keratin, type II cuticular Hb1	1.0000	2.18	1	1	2
Q5474-2	P78385	KRT83_HUMAN	KRT83	Keratin, type II cuticular Hb3	1.0000	2.23	1	1	2
Q5474-3	O43790	KRT86_HUMAN	KRT86	Keratin, type II cuticular Hb6	1.0000	2.26	1	1	2
						LGLEDIETATYR	2	0.9976	2
Q5475-1	O43865-2	SAHH2_HUMAN	AHCYL1	Isoform 2 of Putative adenosylhomocysteinase 2	0.9999	5.8	3	3	3
Q5475-2	O43865	SAHH2_HUMAN	AHCYL1	Putative adenosylhomocysteinase 2	0.9999	5.28	3	3	3

						QVVVCGYGEVVK	2	0.913	1
						TPELTWER	2	0.9921	1
						VVLAEGR	2	0.9833	1
Q5476-1	O60841	IF2P_HUMAN	EIF5B	Eukaryotic translation initiation factor 5B	1.0000	6.48	5	5	6
						HFEATDILVSK	2	0.9753	1
						IPGMILIDTPGHESFSNLR	3	0.9899	2
						LANCELEP	2	0.9516	1
						LKEGDTIVPGVGPVITQIR	3	0.9933	1
						SRINSSGESGDESDFLQSR	2	0.8462	1
Q5477-1	O60884	DNIA2_HUMAN	DNIA2	DnaI homolog subfamily A member 2	0.9781	3.64	1	1	1
						IGLVEALCGQFTFK	2	0.9781	1
Q5478-1	O75083	WDR1_HUMAN	WDR1	WD repeat-containing protein 1	1.0000	44.06	19	20	40
						CFSIDNPGYEPVAVHPGGDTVAIGGVGDNVR	3	0.9987	2
						CVAVGGGYAVVVCIGQVLLKQDR	3	0.9974	4
						DIAWTEDSKR	2	0.9981	2
						DIYTEHAHQVVAK	2	0.9728	1
						FATASADGGIYYDGK	2	0.9997	3
						FGAVFLWDGSSVGEITGHNK	3	0.9967	3
						FTGDGHSR	2	0.9984	1
						GPVTDVAYSIDGAFALVCDASK	3	0.9995	5
						IAVVGGR	2	0.9996	2
						IKDIAWTEGSKR	2	0.9987	2
						IKDIAWTEGSKR	3	0.9854	1
						LATGSDDNCAFFEGPPFK	2	0.999	2
						LYSILGTTLLKDEGK	2	0.9984	2
						NIDNPALADIYTEHAHQVVAK	3	0.9916	2
						NNPSKPLHVIK	2	0.9942	1
						TGSDDNCAFFEGPPFK	2	0.9332	1
						VINSVDIK	2	0.9258	1
						VTVFSVADGYSENNVFGHHAK	3	0.9373	1
						YAPSGFYASGDGVSGK	2	0.9997	3
						YEYQPFAGK	2	0.9981	1
Q5479-1	O75112	LDB3_HUMAN	LDB3	LIM domain-binding protein 3	0.9768	14.03	2	2	2
						GSLVAPSPSPPEARASPTGTPELRPTFSPAFSRPSAFSSSLAEASDGPGRPRASLR	5	0.8527	1
						SSTPIEHAPVCTQATTLPLASAPPPAASPSAASPPLATAAAHTA	4	0.8427	1
Q5480-1	O75351	VPS4B_HUMAN	VPS4B	Vacuolar protein sorting-associated protein 4B	0.9560	3.6	1	1	1
						SLSNKTPTVNEHDLK	3	0.8754	1
Q5481-1	O75494-2	SRS10_HUMAN	SRSF10	Isoform 2 of Serine/arginine-rich splicing factor 10	1.0000	10.34	2	2	6
Q5481-2	O75494-3	SRS10_HUMAN	SRSF10	Isoform 3 of Serine/arginine-rich splicing factor 10	1.0000	14.75	2	2	6
Q5481-3	O75494-4	SRS10_HUMAN	SRSF10	Isoform 4 of Serine/arginine-rich splicing factor 10	1.0000	15.61	2	2	6
Q5481-4	O75494-5	SRS10_HUMAN	SRSF10	Isoform 5 of Serine/arginine-rich splicing factor 10	1.0000	16.36	2	2	6
Q5481-5	O75494-6	SRS10_HUMAN	SRSF10	Isoform 6 of Serine/arginine-rich splicing factor 10	1.0000	14.84	2	2	6
Q5481-6	O75494	SRS10_HUMAN	SRSF10	Serine/arginine-rich splicing factor 10	1.0000	10.31	2	2	6
Q5481-7	Q5JRI1	Q5JRI1_HUMAN	SRSF10	Serine/arginine-rich-splicing factor 10	1.0000	15.7	2	2	6
						GFAYVQVEYVR	2	0.9993	2
						YGPVVDVYVPLDFYTR	2	0.9996	6
Q5482-1	O75531	BAF_HUMAN	BANF1	Barrier-to-autointegration factor	0.9789	13.48	1	1	3
						AYVVLGQFLVLK	2	0.9789	3
Q5483-1	O75534	CSDE1_HUMAN	CSDE1	Cold shock domain-containing protein E1	1.0000	5.01	3	3	5
Q5483-2	O75534-2	CSDE1_HUMAN	CSDE1	Isoform 2 of Cold shock domain-containing protein E1	1.0000	5.22	3	3	5
Q5483-3	O75534-3	CSDE1_HUMAN	CSDE1	Isoform 3 of Cold shock domain-containing protein E1	1.0000	4.92	3	3	5
Q5483-4	O75534-4	CSDE1_HUMAN	CSDE1	Isoform 4 of Cold shock domain-containing protein E1	1.0000	4.74	3	3	5
						ATNIEVLSNTFQFTNEAR	2	0.9994	2
						LLGVVATLK	2	0.9753	1
						LLTSYGFQICSER	2	0.9984	2
Q5484-1	O75594	PGRP1_HUMAN	PGLYRP1	Peptidoglycan recognition protein 1	1.0000	19.9	2	2	5
						AAQQLACGAVAGALR	2	0.9993	3
						YVVVSHTAGSSCNTPASCQQAR	3	0.9904	2
Q5485-1	O75631	UPK3A_HUMAN	UPK3A	Uroplakin-3a	1.0000	31.01	4	4	7
						ASQILNAVLYR	2	0.9992	1
						AVAFDLPSCDPLSDAIGDVSK	2	0.9996	3
						EALGTGHEVLYVLVDISAIR	3	0.9919	2
						VNLQPLQASVTFATNPNTLTVALEKPLCMFDSK	3	0.8699	1
Q5486-1	O75636	FCN3_HUMAN	FCN3	Ficolin-3	1.0000	11.04	3	4	7
Q5486-2	Q5SSB9	Q5SSB9_HUMAN	FCN3	Ficolin-3	1.0000	33.33	3	4	7
Q5486-3	O75636-2	FCN3_HUMAN	FCN3	Isoform 2 of Ficolin-3	1.0000	11.46	3	4	7
						LLGEVDHYQLALGK	2	0.9839	1
						RQDGSVDFFR	2	0.9842	3
						TFAHYATFR	2	0.9936	2
						TFAHYATFR	3	0.9946	1
Q5487-1	O75891-2	AL1L1_HUMAN	ALDH1L1	Isoform 2 of Cytosolic 10-formyltetrahydrofolate dehydrogenase	1.0000	13.98	8	9	17
						ANATEFGLASGVFTR	2	0.9997	2
						DLGEAALNEVLR	2	0.9996	2
						FADGDLDAVLSR	2	0.9995	4
						GAASSVLELAEVLTAEAVR	3	0.9967	4
						IAVIGQSLFGQEVYCHLRK	4	0.8671	1
						MILASNFFK	2	0.9601	1
						SPLIFADCDLNK	2	0.9994	2
						TDVAAPFGGFK	2	0.9467	1
Q5488-1	O75891	AL1L1_HUMAN	ALDH1L1	Cytosolic 10-formyltetrahydrofolate dehydrogenase	1.0000	14.63	10	10	19
Q5488-2	O75891-3	AL1L1_HUMAN	ALDH1L1	Isoform 3 of Cytosolic 10-formyltetrahydrofolate dehydrogenase	1.0000	14.47	10	10	19
						ANATEFGLASGVFTR	2	0.9997	2
						DLGEAALNEVLR	2	0.9996	2
						EEFSGPVMISR	2	0.942	1
						FADGDLDAVLSR	2	0.9995	4
						FLFPEGIK	2	0.9765	1
						GAASSVLELAEVLTAEAVR	3	0.9967	4
						IAVIGQSLFGQEVYCHLRK	4	0.8671	1
						MILASNFFK	2	0.9601	1
						SPLIFADCDLNK	2	0.9994	2
						TDVAAPFGGFK	2	0.9467	1
Q5489-1	O76027	ANXA9_HUMAN	ANXA9	Annexin A9	1.0000	8.41	2	3	7
						ASDSAVDVAIEILATR	2	0.9993	3
						ASDSAVDVAIEILATR	3	0.999	2
						TPPQLQGLAVYK	2	0.9938	2
Q5490-1	O95343	SIX3_HUMAN	SIX3	Homeobox protein SIX3	0.9848	13.86	1	1	1
						SILLASSGGNGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGG	3	0.9495	1
Q5491-1	O95445	APOM_HUMAN	APOM	Apolipoprotein M	0.9998	9.04	2	2	2
Q5491-2	O95445-2	APOM_HUMAN	APOM	Isoform 2 of Apolipoprotein M	0.9998	14.66	2	2	2
						AFLLTPR	2	0.9854	1
						NQAECLSMN	2	0.9919	1
Q5492-1	O95865	DDAH2_HUMAN	DDAH2	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	1.0000	47.37	12	14	27
						AGAGLSLCLVLSTRPH	3	0.8454	1
						AGAGLSLCLVLSTRPHS	2	0.9975	1
						AGAGLSLCLVLSTRPHS	3	0.9941	1
						ALQDLGLR	2	0.9348	1
						DFAVSTVPVSGPSHLR	2	0.9996	3
						DFAVSTVPVSGPSHLR	3	0.9982	1
						EFFVGLSK	2	0.9909	1
						GAEIFADTFR	2	0.9985	2
						GAEIFADTFRDFAVSTVPVSGPSHLR	3	0.9985	3
						GGGDLNPSQALQK	2	0.9996	2
						GVPELASGEGAGAGLPALDLAK	2	0.9996	2
						IVEIGDENATLDGTDVLTGR	2	0.9997	5
						KALQDLGLR	2	0.9989	1
						LSVDTLVPVSCSELEK	2	0.9992	3
Q5493-1	O95954-2	FTCD_HUMAN	FTCD	Isoform C of Formimidoyltransferase-cyclodeaminase	1.0000	21.85	6	7	9
						DQPPAGSQDPGCTGAGLLGDPAGVTVR	3	0.8943	1
						GVSVDECLVCAFAFQR	2	0.9985	2
						LAELDLVPVLYGGAAR	2	0.9967	1
						LGDLSCPFSPK	2	0.9797	1
						NQEVDAISGATQTPGCVLLDWDAGPSTNR	3	0.9664	1
						TYVTVGPPPECVVEGALNAAR	2	0.9984	2

						TVYTFVGPPECVVEGALNAAR	3	0.9894	1
Q5494-1	O9594-4	FTCD_HUMAN	FTCD	Isoform E of Formimidoyltransferase-cyclodeaminase	1.0000	24.05	2	3	5
						GVSVDECVLCAQAFGR	2	0.9985	2
						TVYTFVGPPECVVEGALNAAR	2	0.9984	2
						TVYTFVGPPECVVEGALNAAR	3	0.9894	1
Q5495-1	Q4JM47	Q4JM47_HUMAN	AGR2	AGR2	1.0000	32.82	6	8	13
Q5495-2	O95994	AGR2_HUMAN	AGR2	Anterior gradient protein 2 homolog	1.0000	36.57	6	8	13
						GWGDLQIWTQTYEALYK	2	0.9997	3
						HLSPDGGVYPR	2	0.9917	1
						LAEQFVLLNVYETTDK	2	0.9997	3
						LAEQFVLLNVYETTDK	3	0.9995	2
						LAEQFVLLNVYETTDKHLSPDGGVYPR	3	0.9737	1
						LAEQFVLLNVYETTDKHLSPDGGVYPR	4	0.987	1
						LYAYEPADTALLDNMK	2	0.9969	1
						LYAYEPADTALLDNMK	3	0.9192	1
Q5496-1	O96009	NAPSA_HUMAN	NAPSA	Napsin-A	1.0000	12.14	4	4	7
						FAIQYGTGR	2	0.9995	1
						GCAAILDTGTSITGPTTEIR	2	0.9997	4
						KPIFVPLSNYR	2	0.9135	1
						VGPSLTLCAK	2	0.9875	1
Q5497-1	P00167	CYB5_HUMAN	CYB5A	Cytochrome b5	1.0000	32.09	3	3	6
Q5497-2	P00167-2	CYB5_HUMAN	CYB5A	Isoform 2 of Cytochrome b5	1.0000	43.88	3	3	6
Q5497-3	P00167-3	CYB5_HUMAN	CYB5A	Isoform 3 of Cytochrome b5	1.0000	34.68	3	3	6
						EQAGGDATENFEDVGHSTDAAR	3	0.9629	1
						FLEEHPGGEVLR	2	0.9995	3
						STWLILHHK	2	0.9987	2
Q5498-1	P00338-2	LDHA_HUMAN	LDHA	Isoform 2 of L-lactate dehydrogenase A chain	1.0000	8.76	2	2	4
Q5498-2	P00338-5	LDHA_HUMAN	LDHA	Isoform 5 of L-lactate dehydrogenase A chain	1.0000	9.96	2	2	4
						DLADELALVDVIEDK	2	0.9992	3
						LVITAGAR	2	0.9899	1
Q5499-1	P00338-4	LDHA_HUMAN	LDHA	Isoform 4 of L-lactate dehydrogenase A chain	1.0000	9.12	2	2	4
						DLADELALVDVIEDK	2	0.9992	3
						VTLTSEEAR	2	0.9974	1
Q5500-1	P00338-3	LDHA_HUMAN	LDHA	Isoform 3 of L-lactate dehydrogenase A chain	1.0000	9.42	3	3	5
Q5500-2	P00338	LDHA_HUMAN	LDHA	L-lactate dehydrogenase A chain	1.0000	10.24	3	3	5
						DLADELALVDVIEDK	2	0.9992	3
						LVITAGAR	2	0.9899	1
						VTLTSEEAR	2	0.9974	1
Q5501-1	P00390	GSHR_HUMAN	GSR	Glutathione reductase, mitochondrial	1.0000	4.41	2	2	2
Q5501-2	P00390-3	GSHR_HUMAN	GSR	Isoform 2 of Glutathione reductase, mitochondrial	1.0000	4.67	2	2	2
Q5501-3	P00390-4	GSHR_HUMAN	GSR	Isoform 3 of Glutathione reductase, mitochondrial	1.0000	4.9	2	2	2
Q5501-4	P00390-5	GSHR_HUMAN	GSR	Isoform 4 of Glutathione reductase, mitochondrial	1.0000	5.23	2	2	2
Q5501-5	P00390-2	GSHR_HUMAN	GSR	Isoform Cytoplasmic of Glutathione reductase, mitochondria	1.0000	4.8	2	2	2
						ALLTPVAAGR	2	0.9989	1
						GIYAVSGDVCK	2	0.9721	1
Q5502-1	P00441	SODC_HUMAN	SOD1	Superoxide dismutase [Cu-Zn]	1.0000	71.43	5	5	9
						AVCVLKGDPGVQGIINFQK	3	0.978	1
						GDGPVQGIINFQK	2	0.9741	3
						GLTEGLHGFHVEFGDNTAGCTAGSAGPHFNPLSR	4	0.8768	1
						HVGDGLNVTADKDGVDVSIEDSVISLSDHCIGR	4	0.992	2
						TLVVHEKADDLGKGGNEESTK	3	0.9952	2
Q5503-1	P00488	F13A_HUMAN	F13A1	Coagulation factor XIII A chain	1.0000	3.42	2	2	5
						HVYGELDVQIQR	2	0.9948	3
						MYVAVWTPYGVLR	2	0.9981	2
Q5504-1	P00491	PNPH_HUMAN	PNP	Purine nucleoside phosphorylase	0.9687	3.46	1	1	2
						VFGSLITNK	2	0.9687	2
Q5505-1	P00734	THRB_HUMAN	F2	Prothrombin	1.0000	62.7	116	141	426
						AACLEGNCAEGLTNYR	2	0.9984	5
						ACLEGNCAEGLTNYR	2	0.9983	3
						ADLQENFCR	2	0.9919	3
						ADLQENFCRNPDSSTTGPWCYTTDPTVR	3	0.9663	7
						AEGGLTNYR	2	0.8349	1
						ANTFLEVR	2	0.9055	1
						ATDFWAK	2	0.985	1
						CAEGLTNYR	2	0.9799	1
						CLEGNCAEGLTNYR	2	0.9982	2
						CRNPDSSTTGPWCYTTDPTVR	3	0.9412	1
						CYTDDPTVR	2	0.9121	1
						DKLAACLEGN	2	0.8743	1
						DKLAACLEGNCAE	2	0.9463	1
						DKLAACLEGNCAEG	2	0.9838	1
						DKLAACLEGNCAEGL	2	0.9784	3
						DKLAACLEGNCAEGLG	2	0.8735	1
						DKLAACLEGNCAEGLGT	2	0.884	1
						DKLAACLEGNCAEGLGTN	2	0.9863	2
						DKLAACLEGNCAEGLGTNY	2	0.9888	3
						DKLAACLEGNCAEGLGTNYR	2	0.9996	12
						DKLAACLEGNCAEGLGTNYR	3	0.9995	16
						DLQENFCR	2	0.9867	1
						DSSTTGPWCYTTDPTVR	2	0.9989	7
						EGNCAEGLTNYR	2	0.9867	3
						ELLSYDGR	2	0.9997	8
						ENFCRNPDSSTTGPWCYTTDPTVR	3	0.9587	3
						ENLDRDIALMK	2	0.9973	1
						ETAASLLQAGYK	2	0.9997	1
						ETWTVANVK	2	0.995	1
						FCRNPDSSTTGPWCYTTDPTVR	2	0.9566	2
						FCRNPDSSTTGPWCYTTDPTVR	3	0.9785	4
						GADLQENFCRNPDSSTTGPWCYTTDPTVR	3	0.9484	2
						GDACEGDSGPFVMK	2	0.9997	5
						GIECQLWR	2	0.9794	1
						GNCAEGLTNYR	2	0.9141	1
						GGDQVTVAMTPR	2	0.9788	2
						GPSVLQVNL	2	0.9148	1
						GPSVLQVNLPIVER	2	0.9859	3
						GPSVLQVNLPIVERPV	2	0.9963	1
						GPSVLQVNLPIVERPVCK	2	0.9997	2
						GPSVLQVNLPIVERPVCK	3	0.9992	1
						GPSVLQVNLPIVERPVCKDSTR	3	0.9883	2
						HQDFNSAVQLVENFCR	2	0.9997	4
						HQDFNSAVQLVENFCR	3	0.9997	4
						IECQLWR	2	0.9399	1
						ITDNMFCAGYKPDGK	2	0.9997	3
						ITDNMFCAGYKPDGKR	2	0.9997	3
						ITDNMFCAGYKPDGKR	3	0.9177	1
						IVEGSDAIEGMSFWQVLMFR	3	0.9997	3
						KLAAACLEGNCAEGLTNYR	2	0.9982	3
						KPVAFSDYHVPCLPDRETAASLLQAGYK	3	0.9333	1
						KPVAFSDYHVPCLPDRETAASLLQAGYK	4	0.9893	1
						KSPQELLCGASU	2	0.8909	1
						KSPQELLCGASUSD	2	0.9997	6
						KSPQELLCGASUSD	3	0.9997	5
						LAACLEGNCAEGLTN	2	0.8584	1
						LAACLEGNCAEGLTNY	2	0.9738	2
						LAACLEGNCAEGLTNYR	2	0.9997	12
						LAACLEGNCAEGLTNYR	3	0.9947	2
						LAVTTHGLPLCL	2	0.8756	1
						LAVTTHGLPLCLAWASA	2	0.8434	1
						LAVTTHGLPLCLAWASAQ	2	0.8619	1
						LAVTTHGLPLCLAWASAAQ	2	0.9815	3
						LAVTTHGLPLCLAWASAAQ	2	0.9997	4
						LAVTTHGLPLCLAWASAAQ	3	0.9997	7
						LEGNCAEGLTNYR	2	0.9988	4

						LKKPVAFSDYIHPV	3	0.8441	1
						LKKPVAFSDYIHPVCLPDRETAASLLQAGYK	3	0.9938	2
						LKKPVAFSDYIHPVCLPDRETAASLLQAGYK	4	0.9705	1
						LQENFCR	2	0.9506	1
						LQENFCRNPDSSTTGPWCYTTDPTVR	3	0.9757	5
						LSPPLEQCVPR	2	0.9732	1
						NCAELGNTYR	2	0.9881	1
						NFCRNPDSTTGPWCYTTDPTVR	3	0.9668	3
						NLPIVERPVCK	2	0.9863	1
						NPDGDEGVWCYVAGKPGD	2	0.984	1
						NPDSSTTGPWCYTTD	2	0.9983	3
						NPDSSTTGPWCYTTDPTVR	2	0.9998	16
						NPDSSTTGPWCYTTDPTVR	3	0.9997	5
						NPDSSTTGPWCYTTDPTVRR	2	0.9982	1
						NPDSSTTGPWCYTTDPTVRR	3	0.985	1
						PGADLQENFCR	2	0.9817	1
						PGADLQENFCRNPDSSTTGPWCYTTDPTVR	3	0.965	5
						PWCYTTDPTVR	2	0.9731	2
						QECSIPVCGQDQVTVAMTPR	2	0.9997	6
						QECSIPVCGQDQVTVAMTPR	3	0.9996	2
						RGDACEGDSGGPFVVK	2	0.9985	1
						RGDACEGDSGGPFVVK	3	0.9785	1
						RNPDSSTTGPWCYTTDPTVR	2	0.9965	3
						RNPDSSTTGPWCYTTDPTVR	3	0.9923	2
						RQECIPVCG	2	0.8759	1
						RQECIPVCGQ	2	0.9119	1
						RQECIPVCGQD	2	0.9889	2
						RQECIPVCGQDQ	2	0.9989	7
						RQECIPVCGQDQVT	2	0.9988	5
						RQECIPVCGQDQVTV	2	0.9981	5
						RQECIPVCGQDQVTV	2	0.998	6
						RQECIPVCGQDQVTVAM	2	0.8554	1
						RQECIPVCGQDQVTVAMTPR	2	0.9519	1
						RQECIPVCGQDQVTVAMTPR	2	0.9997	9
						RQECIPVCGQDQVTVAMTPR	3	0.9997	16
						SEGSSVNLSPLEQCVPR	2	0.9997	7
						SEGSSVNLSPLEQCVPR	3	0.9985	1
						SEGSSVNLSPLEQCVPRDG	2	0.9736	2
						SEGSSVNLSPLEQCVPRDGGQY	2	0.9171	1
						SEGSSVNLSPLEQCVPRDGGQYQGR	3	0.9963	4
						SGIECQLW	2	0.9776	1
						SGIECQLWR	2	0.9997	9
						SGIECQLWR	3	0.9843	1
						SIPVCGQDQVTVAMTPR	2	0.9989	5
						SIPVCGQDQVTVAMTPR	3	0.9642	1
						SLEDKTERELLESYDGR	3	0.9994	6
						SPPLEQCVPR	2	0.9557	3
						SPQELLCASUSDR	2	0.9998	7
						SPQELLCASUSDR	3	0.9949	1
						SRYPHKPEINSTHPGADLQENFCR	3	0.9262	1
						SRYPHKPEINSTHPGADLQENFCR	4	0.9682	1
						SSTTGPWCYTTDPTVR	2	0.9989	3
						STATDVFWAK	2	0.9585	1
						STTGPWCYTTDPTVR	2	0.9986	3
						STTHPGADLQENFCR	2	0.9989	5
						STTHPGADLQENFCR	3	0.9776	3
						STTHPGADLQENFCRNPDSSTTGPWCYTTDPTVR	3	0.9617	3
						TATDVFWAK	2	0.9794	1
						TFGSGEADCGLRPL	2	0.9925	3
						TFGSGEADCGLRPLF	2	0.9865	4
						TFGSGEADCGLRPLFE	2	0.9784	1
						TFGSGEADCGLRPLFEK	2	0.9997	5
						TFGSGEADCGLRPLFEK	3	0.9994	1
						TFGSGEADCGLRPLFEKK	2	0.9997	4
						TFGSGEADCGLRPLFEKK	4	0.9974	3
						TGPWCYTTDPTVR	2	0.9978	3
						TPRDKLAALCGNCAELGTNVR	3	0.9992	3
						TTPWCYTTDPTVR	2	0.9979	3
						TTHPGADLQENFCR	3	0.9712	1
						VNLPIVERPVCK	2	0.9462	2
						VTGWGNLK	2	0.9932	2
						VTGWGNLKETWTANVGK	2	0.9995	3
						VTGWGNLKETWTANVGK	3	0.9988	2
						WVLTAH	2	0.8499	1
						YTTDPTVR	2	0.9549	2
Q5506-1	P00739	HPTR_HUMAN	HPR	Haptoglobin-related protein	1.0000	26.15	8	8	12
Q5506-2	P00739-2	HPTR_HUMAN	HPR	Isoform 2 of Haptoglobin-related protein	1.0000	23.64	8	8	12
						AVGDKLPECEAVCGKPK	2	0.997	2
						GSFPWQAK	2	0.9876	1
						ILGGHLDK	2	0.9991	1
						LRTGGGVVTLNDKK	3	0.9803	1
						SCAVAEKVGVK	2	0.9997	4
						SPVGVQPLNENFTCVGMSK	3	0.9365	1
						TEGDGVYTLNDKK	2	0.9996	1
						VTSIQHWVQK	2	0.9648	1
Q5507-1	P00740	FA9_HUMAN	F9	Coagulation factor IX	1.0000	23.64	9	11	22
						FGSGYVSGWGR	2	0.9992	2
						ITVAGEHNIEETEIQK	3	0.9931	2
						NCELDVTCNIK	2	0.9993	1
						NSADNKKVCSCTEGYR	2	0.9985	2
						NSADNKKVCSCTEGYR	3	0.8358	1
						SCEPAVPFPCGR	2	0.9997	3
						SYECWCPFGFEK	2	0.9957	3
						VDAFCGGSVINER	2	0.9996	3
						VVCSCTEGYR	2	0.99	1
						WIVTAACHVETGVK	2	0.9996	3
						WIVTAACHVETGVK	3	0.9349	1
Q5508-1	P00740-2	FA9_HUMAN	F9	Isoform 2 of Coagulation factor IX	1.0000	8.75	3	3	8
						FGSGYVSGWGR	2	0.9992	2
						SCEPAVPFPCGR	2	0.9997	3
						WIVTAACHVETGVK	2	0.9996	3
Q5509-1	P00742	FA10_HUMAN	F10	Coagulation factor X	1.0000	24.18	11	14	27
						ACIPTGYPYCGK	2	0.9997	2
						ACIPTGYPYCGKQ	2	0.9304	2
						ETYDFDIAVLR	2	0.9997	3
						ETYDFDIAVLR	3	0.9426	1
						FKDTYTYTGIVSWGEGCAR	3	0.9988	2
						FTKETDYDFDIAVLR	2	0.9996	2
						FTKETDYDFDIAVLR	3	0.9993	2
						GYTLADNGK	2	0.9992	1
						LSSFIITQNMFCAGYDTK	2	0.9996	4
						MLEVPYVDR	2	0.9993	1
						NCELFTR	2	0.9992	2
						NTEQEEGGAEVHEVEVIK	2	0.9997	2
						NTEQEEGGAEVHEVEVIK	3	0.9995	2
						TGIVSGFGR	2	0.9996	1
Q5510-1	P00747	PLMN_HUMAN	PLG	Plasminogen	1.0000	59.51	58	68	149
						ATTVTGTGTCQDWAAGEPHR	2	0.9998	3
						ATTVTGTGTCQDWAAGEPHR	3	0.9996	1
						CEQDEFTFR	2	0.9986	3
						CQSWSSMTPHR	2	0.9982	2
						CQSWSSMTPHR	3	0.9558	1
						CTTPPPSSGPTYQCLK	2	0.9993	3

						DVVLFEKK	2	0.9304	1
						EAQLPVIENK	2	0.9995	2
						ELRPWCFTDPNK	2	0.8957	1
						ELRPWCFTDPNKR	2	0.964	1
						ELRPWCFTDPNKR	3	0.999	2
						EQCCVIMAEKNR	2	0.9992	1
						EQCCVIMAEKNR	2	0.9985	2
						FSPATHPSEGLEENYCR	2	0.9997	2
						FSPATHPSEGLEENYCR	3	0.9621	1
						FVTWIEGVMR	2	0.9996	4
						HSIFTPETNPR	2	0.9997	4
						HSIFTPETNPR	3	0.9989	1
						KLYDYCDVPQCA	2	0.9956	1
						KLYDYCDVPQCAA	2	0.8058	1
						KLYDYCDVPQCAAPSFDCGKPKQVEP	3	0.8157	1
						KLYDYCDVPQCAAPSFDCGKPKQVEPK	3	0.9997	6
						KQLGAGSIEECAAK	2	0.9995	2
						KSSIIR	2	0.991	2
						KVYLSECK	2	0.9951	1
						LFLFETR	2	0.9982	1
						LGAGSIEECAAK	2	0.9018	1
						LSSPAVITOK	2	0.9992	1
						LSSPAVITOKVIPACLPSPNYVADRTCEFTGWGETQGTGAGLLK	4	0.8369	1
						LYDYCDVPQCAAPSFDCGKPKQVEPK	3	0.9973	1
						MRDVLFEK	3	0.9709	2
						NLDENYCR	2	0.9993	1
						NLDENYCRNPDGKR	2	0.9915	1
						NLEPHVQIEVSR	2	0.899	1
						NPDAADGKPCWCFITDPSVR	2	0.9996	4
						NPDAADGKPCWCFITDPSVR	3	0.9992	4
						NPDGDDVGGPWCTTNNPR	2	0.9998	6
						NPDNDPGGPNCTTDPKRR	3	0.9993	3
						NYCRNPDGDDVGGPWCTTNNPR	2	0.9996	5
						NYCRNPDGDDVGGPWCTTNNPR	3	0.9995	9
						PDVETPSEEDCMFGNGK	2	0.9985	3
						QLGAGSIEECAAK	2	0.9994	2
						RAPWCHTTSQVR	2	0.9981	2
						RAPWCHTTSQVR	3	0.9874	1
						RATTVTGTGTCQDWAAGEPHR	3	0.9996	3
						RWELCDIPR	2	0.9957	2
						SIFTPETNPR	2	0.9361	1
						TECHITGWGETQGTGAGLLK	2	0.9997	4
						TECHITGWGETQGTGAGLLK	3	0.9965	2
						TPENFCIK	2	0.9996	1
						TPENYPMAGLTNNYCR	2	0.9997	3
						VCNRYEFLNGR	2	0.9464	2
						VCNRYEFLNGR	3	0.9787	1
						VETPSEEDCMFGNGK	2	0.9906	2
						VGGPWCTTNNPR	2	0.9266	1
						VILGAHQEVNLEPHVQIEVSR	3	0.9997	4
						VIPACLPSPNYVADRTCEFTGWGETQGTGAGLLK	2	0.9997	6
						VIPACLPSPNYVADRTCEFTGWGETQGTGAGLLK	3	0.8951	1
						VQDCYHGDGQSYR	2	0.9974	2
						VQSTELCAGHLAG	2	0.9476	1
						VQSTELCAGHLAGG	2	0.9587	1
						VQSTELCAGHLAGGT	2	0.9694	1
						VQSTELCAGHLAGGTD	2	0.9894	2
						VQSTELCAGHLAGGTD	2	0.9525	1
						VQSTELCAGHLAGGTDSCGDDSGGPLVCFEK	3	0.9995	3
						VYLSECK	2	0.994	1
						WELCDIPR	2	0.9997	3
						YILQGVTSWGLGCRPNKPGVYVR	3	0.9964	3
Q5511-1	P00748	FA12_HUMAN	F12	Coagulation factor XII	1.0000	17.89	10	11	24
						CPEQLLR	2	0.9867	1
						CLEVEGHR	2	0.9993	1
						DVAYYLAWIR	2	0.9916	2
						LHEAFSPVSVQHDALLR	3	0.9995	2
						LLOGISWGGSGGCDR	2	0.9995	4
						NRPGVYTDVAYYLAWIR	2	0.9996	3
						NRPGVYTDVAYYLAWIR	3	0.9995	4
						NPONDIPRPWCVLNR	3	0.9482	1
						RLTLOGISWGGSGGCDR	3	0.9959	1
						TTLGAPCPQWASEATYR	2	0.9997	3
						VVGLVALR	2	0.9993	2
Q5512-1	P00918	CAH2_HUMAN	CA2	Carbonic anhydrase 2	0.9999	9.62	2	2	2
						AVQQPDGLAVLGFILK	2	0.9148	1
						VVDVLDISK	2	0.9382	1
Q5513-1	P00966	ASSY_HUMAN	ASS1	Argininosuccinate synthase	1.0000	74.76	29	33	58
						AELVYTGFWHSPECFVR	2	0.9084	1
						APNTPDILEIEFK	2	0.9996	3
						EFVEEFWPAICSSALYEDR	3	0.9997	6
						EGQYDVIAIANIGQEK	2	0.9996	1
						EGQYDVIAIANIGQEKEDFEAR	3	0.9702	2
						ESPLSLNLEYLMNMYGQDYEPDGTGFININSLR	3	0.9994	3
						FAELVYTGFWHSPECFVR	2	0.9997	2
						FAELVYTGFWHSPECFVR	3	0.9362	2
						FELSCYSLAPQIK	2	0.9997	3
						FELSCYSLAPQIK	3	0.8958	1
						FELSCYSLAPQIKV	2	0.977	2
						GIYETPAGTILYH	2	0.9658	2
						GIYETPAGTILYHAHLDEAFTMDR	3	0.8278	1
						GNDQVRFELSCYSLAPQIK	3	0.8655	1
						GQVYILGR	2	0.9986	2
						GRNDLMEYAK	2	0.9436	2
						IDIVENR	2	0.9922	1
						KVFIEDVSR	2	0.9952	2
						KVFIEDVSR	3	0.9988	1
						MPEFYNR	2	0.9976	1
						NDLMEYAK	2	0.9963	1
						NPWSMDENLMHSYEAGILENPK	3	0.999	4
						NQAPPGLYTK	2	0.9967	1
						QHGIPIPVTPK	2	0.9801	1
						SGGLDTSCLVWLK	2	0.9741	1
						SYEAGILENPK	2	0.9797	1
						TQDPAKAPNTPDILEIEFK	3	0.9983	3
						TQDPAKAPNTPDILEIEFKK	3	0.9237	1
						VQDVSLK	2	0.9935	1
						VTNVKDGTTHTSLELFMYNLEVAGK	3	0.9926	1
						YLLGTSLAR	2	0.8694	1
						YLLGTSLARPCIR	2	0.9971	2
						YLLGTSLARPCIR	3	0.902	1
Q5514-1	P01008	ANT3_HUMAN	SERPINC1	Antithrombin-III	1.0000	60.13	27	35	70
						ADGESCSASMMYQEGK	2	0.9996	2
						AFLEVNEEGSEAAASTAVVIAGR	2	0.9997	3
						AFLEVNEEGSEAAASTAVVIAGR	3	0.9994	4
						ANRPFVIFR	2	0.9993	2
						ANRPFVIFR	3	0.9996	3
						ATEDEGSEQIPEATNR	2	0.9996	2
						ATEDEGSEQIPEATNR	3	0.9519	1
						DDLYSDAFHK	2	0.9996	1
						DIPMNPVCMYR	2	0.9976	1
						EQLODMGLVDLFSPEK	2	0.9997	5
						EQLODMGLVDLFSPEK	3	0.9705	1

						EVPLNTIIFMGR	2	0.9996	3
						FATTFYQHLDASK	2	0.999	3
						FATTFYQHLDASKNDNDNIFLSPISSTAFAMTK	3	0.9979	2
						FRIEDGFSLK	2	0.9469	1
						FRIEDGFSLK	3	0.999	3
						FRIEDGFSLKEQLQDMGLVDFSPK	3	0.9966	2
						GSVPDICTAKPR	2	0.8451	1
						IEDGFSLKQLQDMGLVDFSPK	3	0.8954	2
						ITDVIPEAINELTVLVNNTYFK	2	0.9997	3
						ITDVIPEAINELTVLVNNTYFK	3	0.9995	3
						LQPLDFKENAEQSR	2	0.9983	2
						NDNDNIFLSPISSTAFAMTK	2	0.9996	2
						RVAEGTQVLELPFKGDDITMVILPKPEK	4	0.9328	1
						RVWELSK	2	0.9933	1
						SKLPGIVAAGR	2	0.9922	1
						SKLPGIVAAGR	3	0.8738	1
						SKLPGIVAEGRDDLYSDAFHK	4	0.9619	2
						SLNPNRVTFK	2	0.9378	1
						SPVDICTAKPR	2	0.9549	1
						TSQDIHFFAK	2	0.9996	3
						TSQDIHFFAK	3	0.9711	1
						VAEGTQVLELPFK	2	0.9995	3
						VAEGTQVLELPFKG	2	0.9691	2
						VAEGTQVLELPFKGDDITMVILPKPEK	3	0.9969	1
Q5515-1	P01009	A1AT_HUMAN	SERPINA1	Alpha-1-antitrypsin	1.0000	69.86	47	58	120
						ALVNYIFFK	2	0.8542	1
						AVLTIDEK	2	0.9995	2
						DTEEDFHVD	2	0.9957	3
						DTEEDFHVDQV	2	0.8215	1
						DTEEDFHVDQVTVK	2	0.9997	2
						DTVFALVNIWFK	2	0.9996	3
						ELDRDTVFALVNIWFK	2	0.9545	1
						ELDRDTVFALVNIWFK	2	0.9979	2
						ELDRDTVFALVNIWFK	3	0.9992	3
						FFLPDEGK	2	0.9838	2
						FLNEDR	2	0.976	1
						FNKPFVF	2	0.9763	1
						FNKPFVFL	2	0.9853	3
						FNKPFVFLMIEQNTK	2	0.9996	3
						FNKPFVFLMIEQNTK	3	0.9995	3
						GKWERPFEVK	2	0.9023	1
						GTEAGAMFLAIPMSIPFEVK	3	0.9862	2
						ITPNLAFAF	2	0.8964	1
						ITPNLAFAFSLYR	2	0.9998	6
						ITPNLAFAFSLYR	3	0.9997	5
						KLSSWVLLMK	2	0.9862	3
						KLSSWVLLMK	3	0.9975	2
						KQINDYVEK	2	0.9943	2
						LAFAFSLYR	2	0.9971	3
						LGMFNIQH	2	0.9786	2
						LGMFNIQHCK	2	0.9911	2
						LQHLENLTH	2	0.971	1
						LQHLENLTHDIITK	2	0.9997	3
						LQHLENLTHDIITK	3	0.9992	1
						LQHLENLTHDIITK	4	0.9593	1
						LSGVTEAPLK	2	0.954	1
						LSVSTHDLK	2	0.9997	6
						LSSWVLLMK	2	0.9996	3
						LVDKFLEDVK	2	0.9729	1
						LVDKFLEDVK	3	0.9812	1
						LVDKFLEDVKK	2	0.9978	2
						LVDKFLEDVKK	3	0.9984	1
						LYHSEFTVNFQDTEAK	3	0.9436	1
						LYHSEFTVNFQDTEAKK	3	0.9991	3
						LYHSEFTVNFQDTEAKK	4	0.9749	1
						NLAFAFSLYR	2	0.9367	2
						QINDYVEK	2	0.9602	1
						QINDYVEKGTQK	2	0.9963	2
						SASULPK	2	0.9995	3
						SASULPKL	2	0.9646	3
						SPLFMKG	2	0.9995	1
						SPVSIATAFAMLSLGTK	3	0.9295	1
						SVLGQLGITK	2	0.9997	3
						SVLGQLGITKV	2	0.9849	1
						TAFAMLSLGTK	2	0.8751	1
						TLNQPDSQLQTLTGNGLFSLGLK	2	0.9985	1
						TLNQPDSQLQTLTGNGLFSLGLK	3	0.9963	1
						VFSNGADLSGVTEAPLK	2	0.9997	5
						VFSNGADLSGVTEAPLKL	2	0.9694	2
						VFSNGADLSGVTEAPLKLK	2	0.9974	2
						VFSNGADLSGVTEAPLKLK	3	0.9966	3
						WERPFEVK	2	0.8973	1
						WERPFEVK	2	0.8846	1
Q5516-1	P01011	AACT_HUMAN	SERPINA3	Alpha-1-antichymotrypsin	1.0000	38.06	15	16	36
						ADLSGITGAR	2	0.9993	3
						AVLDVFEEGTEASAATAVK	2	0.9997	4
						AVLDVFEEGTEASAATAVK	3	0.9946	1
						DEELSCTVVELK	2	0.9992	3
						DVFEEGTEASAATAVK	2	0.9969	2
						DYNLDILLQLGIEEAFISK	2	0.9958	1
						EIGELYLPK	2	0.9982	2
						EIGELYLPKF	2	0.9863	1
						EQLSLLR	2	0.9332	1
						FNRPFLMIIVPTDTGNIFMSK	3	0.9991	5
						GTHVDGLASAVVDFSLYK	3	0.9966	2
						ITLSALVETR	2	0.9997	3
						LYGSEAFATFDQDSAAK	2	0.9995	3
						NLAVSQVHK	2	0.9969	2
						TLSALVETR	2	0.8869	1
						VFEEGTEASAATAVK	2	0.9874	2
Q5517-1	P01023	A2MG_HUMAN	A2M	Alpha-2-macroglobulin	1.0000	29.04	39	41	77
						AAQVTIQSSGTFSSK	2	0.9993	2
						AFQPFVELTMPYSVIR	2	0.9995	3
						AGAFCLSEDAGLIGISTASLR	2	0.9985	2
						AIQVLTGYQR	2	0.9986	1
						ALFCLSAWK	2	0.966	2
						ALLEIPVTHPVVR	2	0.9821	3
						AQIQEGTVVELTGR	2	0.9866	3
						AYIFIDEAHITQ	2	0.9588	2
						AYIFIDEAHITQ	2	0.9796	2
						AYIFIDEAHITQALIVLSQR	3	0.9994	5
						DLKPAIVK	2	0.9863	1
						FEVQVTPK	2	0.9878	1
						FSGQLNSHGCFYQVVK	3	0.9635	1
						GEAFTLK	2	0.9821	1
						GEAFTLKA	2	0.9521	1
						GGVEDEVTL SAYTIALLEIPVTHPVVR	3	0.9959	1
						IAQWQSFQLEGGLK	2	0.9995	2
						ITALLEIPVTHPVVR	3	0.8933	1
						LHTEAQIQEGTVVELTGR	3	0.999	2
						LPPNVVESAR	2	0.9705	1
						LHVVEPHTETVR	2	0.9994	2
						NALFCLSAWK	2	0.9988	3

						NEDSLVFVQTDK	2	0.9992	2
						NGQNTWLTAFVLK	2	0.9994	3
						QSFPLSSEPQGSYK	2	0.998	2
						QGIPIFFGQVR	2	0.9935	2
						RVTAAPQSVCLAR	2	0.9882	2
						SDIAPVAR	2	0.9369	1
						SLFTDLAENDVLH	2	0.9888	3
						SLFTDLAENDVLHCYAFVAPK	2	0.9905	1
						SLFTDLAENDVLHCYAFVAPK	3	0.999	2
						SSGSLNNAIK	2	0.9936	1
						TEHPTVEEFVLK	2	0.9914	2
						TEHPTVEEFVLK	3	0.9346	1
						TGTHGLLVK	2	0.9992	2
						VGYESDVMMGR	2	0.9985	2
						VSVQLEASPAFLAVPEK	2	0.9991	3
						VTAAPQSVCLAR	2	0.9988	1
						VTGEGCVLTLSLK	2	0.9992	3
						VVSMDENHPLNELPLVYIQDPK	3	0.997	1
Q5518-1	P01024	CO3_HUMAN	C3	Complement C3	1.0000	YDVENCANLK	2	0.9588	1
						64.4	147	175	397
						AAVYHHFISDGVR	2	0.9997	3
						AAVYHHFISDGVR	3	0.9995	3
						AAVYHHFISDGVRK	2	0.9961	1
						AAVYHHFISDGVRK	3	0.9991	3
						ACEPGVDVYVK	2	0.9991	1
						ACEPGVDVYVK	2	0.8916	1
						ADIGCTPGSGK	2	0.9839	1
						AEDLVGK	2	0.9984	1
						AFVIFGIQDGEQR	2	0.919	1
						AFVLISLQEAQ	2	0.8951	1
						AGDFLEANYMNLQR	2	0.9997	4
						AKDQLTCNKFDLK	2	0.9993	3
						ALLALLQLK	2	0.9582	1
						ALLQLKDFDVPVVR	2	0.9134	2
						APSTWLTAYVVK	2	0.9992	2
						ASHLGLAR	2	0.998	1
						AVHYLDETEQWEK	2	0.9639	2
						AVYHHFISDGVR	2	0.9948	3
						AVYHHFISDGVR	3	0.9631	1
						AYYENSQQQVSTFEVK	2	0.9997	6
						AYYENSQQQVSTFEVK	3	0.999	3
						AYYNLEESCTR	2	0.9915	1
						AYYTLIGASGQR	2	0.9886	2
						CAENECIDK	2	0.9997	1
						DAPDHQELNLDVSLQPSR	3	0.9985	2
						DEDIAEENIVSR	2	0.9562	1
						DFDFVPPVVR	2	0.9996	2
						DICEQVNSLPGSITK	2	0.9997	4
						DKVSHSDDCLAFK	2	0.9568	3
						DQLTCNKFDLK	2	0.9693	1
						DSCVGSLLVK	2	0.9994	2
						DSITTWEILAVMSDKK	2	0.9993	1
						DTWVEHWPEEDCQDEENQK	3	0.9995	3
						DVSLQLPSR	2	0.9861	2
						DYAGVFSAGLFTSSSGQQTAAQR	3	0.98	2
						EALKLEK	2	0.9763	1
						ENEGFTVTAQK	2	0.9704	2
						EPGQDLVVLPLSITTDIPFSR	2	0.9997	5
						EPGQDLVVLPLSITTDIPFSR	3	0.9842	2
						EVVADSVVVDVKD	2	0.9959	2
						EYVLPSEFIVEPTEK	2	0.9997	4
						EYVLPSEFIVEPTEK	3	0.9581	1
						EYVLPSEFIVEPTEKF	2	0.929	1
						FDEYIMAEQTIK	2	0.9483	2
						FVTVQATFGTQVVEK	2	0.9989	2
						FYYINKE	2	0.9994	2
						GICVADPFVTVMQQDFIDLR	2	0.9997	2
						GLEVITITAR	2	0.9997	3
						GGQTLSSVMTMHAHAK	2	0.9997	2
						GGQTLSSVMTMHAHAK	3	0.9629	1
						GVYVLNKK	2	0.9412	1
						GYTQQLAFR	2	0.9913	1
						HFISDGVR	2	0.8323	1
						HYLDETEQWEK	2	0.9919	2
						IHWESASLLR	2	0.9995	2
						IHWESASLLR	3	0.9995	4
						IIAEENIVSR	2	0.8286	1
						ILQGTPVAQMTEDAVDAER	2	0.9986	1
						ILQGTPVAQMTEDAVDAER	3	0.9889	1
						ILQGTPVAQMTEDAVDAERLK	3	0.9136	1
						IPIEDSGSEVLSR	2	0.9997	8
						ISLPSLKR	2	0.9794	1
						ISLQEAQ	2	0.8934	1
						IWDVVEK	2	0.9736	1
						KACEPGVDVYVK	2	0.8292	1
						KGYTQQLAFR	2	0.9982	1
						KQELSEAEQATR	2	0.9995	5
						KQELSEAEQATR	3	0.9183	1
						KVEGTAFVIFGIQDGEQR	3	0.9993	8
						KVLLDGVQNP	2	0.9994	3
						KVLLDGVQNP	3	0.9954	2
						LKACEPGVDVYVK	2	0.9989	3
						LKACEPGVDVYVK	3	0.8931	1
						LESEETMVLFAH	2	0.8348	1
						LESEETMVLFAHD	2	0.9332	2
						LESEETMVLFAHDAGQ	2	0.928	1
						LESEETMVLFAHDAGQDVPVTV	2	0.8127	1
						LESEETMVLFAHDAGQDVPVTVTVHDFPGK	3	0.9996	3
						LESEETMVLFAHDAGQDVPVTVTVHDFPGK	4	0.9971	1
						LKGPLLNK	2	0.8267	1
						LPYSVVR	2	0.9989	2
						LPYSVVRNEQVEIR	3	0.9935	1
						LSINTHPSQKPLSITVR	2	0.9956	1
						LSINTHPSQKPLSITVR	3	0.998	2
						LVAYYTLIGASGQR	2	0.9997	7
						LVAYYTLIGASGQR	3	0.9996	4
						NUNADSDVLCGAVK	2	0.99	4
						NNNEKDMALTAFLVLSLQEAQ	3	0.9826	2
						NTLIYLDK	2	0.9954	2
						NTLIYLDKVSSEDCLAFK	3	0.991	2
						NTMILEICTR	2	0.9997	3
						PLSITTDIPFSR	2	0.9773	1
						QCQDLGAFTESMVVFGCPN	2	0.9995	2
						QELSEAEQATR	2	0.9985	2
						QGAELEIK	2	0.9965	1
						QVREPGQDLVVLPLSITTDIPFSR	3	0.9978	6
						RAPSTWLTAYVVK	2	0.9484	1
						RAPSTWLTAYVVK	3	0.8601	1
						RIFTVINHR	2	0.9326	1
						RIHWESASLLR	3	0.9687	1
						RIPEDGSGEVLSR	2	0.9993	5
						RIPEDGSGEVLSR	3	0.9987	2
						RLVAYYTLIGASGQR	2	0.9888	3

						RLVAYYTLGASGQR	3	0.8417	1
						SDAGLFTSSSGQQTAR	2	0.9935	2
						SDDKVTLEER	2	0.9993	10
						SEETKENEGFTVTAEGK	2	0.9996	3
						SEETKENEGFTVTAEGK	3	0.9994	2
						SGIPVYSPQCHFH	2	0.9867	2
						SGIPVYSPQCHFH	2	0.9997	3
						SGQSEDRQPVPGQOMTLK	2	0.9993	3
						SGSDEVQVGQQR	2	0.9996	4
						SITTFIPFSR	2	0.9822	2
						SLOGYLFQTDK	2	0.9923	3
						SLYVSATVILHSGSDMVQAER	3	0.9473	1
						SNLDEDAEENIVSR	2	0.9997	7
						SNLDEDAEENIVSR	3	0.9967	3
						SPQQVFSTFEVK	2	0.9646	2
						SSLVPPYVIVPLK	2	0.9995	3
						SYALLALLQLK	2	0.9476	2
						SYTVAIAGYALAQMR	2	0.9995	3
						SYTVAIAGYALAQMR	3	0.9937	2
						TELRPGETL	2	0.89	1
						TELRPGETLVN	2	0.9835	2
						TELRPGETLVN	2	0.9872	1
						TELRPGETLVN	2	0.9969	3
						TELRPGETLVN	2	0.9993	4
						TELRPGETLVN	3	0.9997	9
						TFISPIK	2	0.9968	1
						TFISPIK	2	0.8338	1
						TGLQEVVK	2	0.9997	2
						TGLQEVKA	2	0.9928	1
						TIYTPGSTVLY	2	0.9899	1
						TIYTPGSTVLYR	2	0.9986	2
						TKNQLESAEQATR	2	0.9989	3
						TYMVNIENPEGIPYK	2	0.9358	1
						VAYYTLGASGQR	2	0.8481	1
						VEGTAFFVIGIQDGEQR	2	0.9994	6
						VEGTAFFVIGIQDGEQR	3	0.8989	1
						VELLHNPAFCSL	2	0.8501	1
						VELLHNPAFCSLATTK	2	0.9996	2
						VELLHNPAFCSLATTK	3	0.9956	3
						VFLDCCNVITELR	2	0.9994	2
						VHQYFNVELIQPGAVK	2	0.9997	3
						VHQYFNVELIQPGAVK	3	0.9995	4
						VIFGIQDGEQR	2	0.8066	1
						VILSLQEA	2	0.9639	2
						VLDGQDNBR	2	0.9995	4
						VLPISITTDIPFSR	2	0.9562	1
						VLPSEVIVEPTEK	2	0.8929	1
						VQLSNDFDEYIMAEQTIK	2	0.9997	8
						VQLSNDFDEYIMAEQTIK	3	0.9996	4
						VSHSEDDCLAFK	2	0.9986	2
						VSHSEDDCLAFK	3	0.9972	1
						VTIKPAPETEK	2	0.9948	1
						VTIKPAPETEK	3	0.9933	1
						VTIKPAPETEKRPQDAK	3	0.8802	2
						VVLVAVDK	2	0.9995	2
						VVLVAVDKGVFLNK	3	0.9938	2
						VVLVAVDKGVFLNKK	3	0.9989	2
						VYAYNLEESCTR	2	0.9997	5
						VYAYNLEESCTR	2	0.8516	1
						VYHHFISDGV	2	0.9538	2
						VYAYNLEESCTR	2	0.9903	3
						YENSPOQVFSTFEVK	2	0.9757	1
						YISKYELDK	2	0.9784	1
						YISKYELDKAFSDR	3	0.9911	2
						YNLEESCTR	2	0.9332	2
						YSIITPNILR	2	0.9689	1
						YTLGASGQR	2	0.9938	1
						YGGGYGSTQATF	2	0.938	1
						YGGGYGSTQATFMMVQALAQYK	3	0.9996	4
						YNLEESCTR	2	0.9785	3
						YTYLUGASGQR	2	0.9279	1
						YTYLIMNK	2	0.9995	2
Q5519-1	P01031	CO5_HUMAN	C5	Complement C5	1.0000	13.84	19	20	32
						AFTECCVVASQLR	2	0.9846	1
						ALLVGEHLNIIVTPK	3	0.9978	2
						ATLLDIYK	2	0.9678	1
						DINYVNPVIK	2	0.9804	1
						ELSYLSLEDLNNK	2	0.9985	3
						ENSLYLTAFTVIGIR	2	0.9995	3
						ENSLYLTAFTVIGIR	3	0.9958	1
						ENSLYLTAFTVIGIRK	2	0.8992	1
						GGASSTWATFALR	2	0.9959	2
						IDTALIK	2	0.9007	1
						IVACASYKPSR	2	0.9986	1
						KAFDICPLVK	2	0.9925	2
						LLVYVITGEQTALVSDSVLNIEK	3	0.9984	2
						LPYSVVR	2	0.9989	2
						LQGTLPVEAR	2	0.9877	1
						SYFPESWLWEVHLVPR	3	0.9423	1
						TDAPDLPEENQAR	2	0.9983	2
						TSTSEEVCSFYLK	2	0.9995	3
						VSITSITVENVFVK	2	0.9616	1
						YIYPLDSLWIEWPR	2	0.9031	1
Q5520-1	P01034	CYT_C_HUMAN	CST3	Cystatin-C	0.9864	16.44	2	2	3
						AGVNYFLDVELR	2	0.821	1
						ALDFAVGEYIK	2	0.9829	2
Q5521-1	P01042-2	KNG1_HUMAN	KNG1	Isoform LMW of Kininogen-1	1.0000	45.9	27	31	70
						DFVQPTTK	2	0.9592	1
						DIPTNSPELEETLTHITTK	2	0.9997	4
						EGDCPVQSGKTWQDCEYKDAK	3	0.9822	2
						ENFLFLTPDCK	2	0.9996	2
						ESNEELTESCETK	2	0.9997	2
						ESNEELTESCETK	2	0.9992	3
						ETTCSEKNEELTESCETK	2	0.9995	3
						ETTCSEKNEELTESCETK	3	0.9921	1
						ETTCSEKNEELTESCETK	3	0.9836	2
						IASFSQNCDIYFGK	2	0.9995	2
						IASFSQNCDIYFGK	2	0.8871	1
						IASFSQNCDIYFGKDFVQPTTK	3	0.999	7
						IGEIKETTSHLR	2	0.9995	2
						IGEIKETTSHLR	3	0.9988	1
						KLQSLDCNAEYVVPWEK	2	0.9997	2
						KLQSLDCNAEYVVPWEK	3	0.986	2
						KYFIDFVAR	2	0.9993	3
						KYFIDFVAR	3	0.9991	1
						KYNSQNSQNSQNFVLYR	2	0.9997	2
						LGQSLDCNAEYVVPWEK	2	0.9997	4
						LGQSLDCNAEYVVPWEK	3	0.9992	2
						QVYAGLNFR	2	0.9996	1
						SLWNGDTGCTCDNAYIDIQLR	2	0.9997	3
						TVGSOTFYSFK	2	0.9996	1
						TVGSOTFYSFKYEIK	2	0.9992	3
						TVGSOTFYSFKYEIK	3	0.8514	1

Q5533-1	P01743	HV102_HUMAN		lg heavy chain V-I region HG3	0.9333	9.4	1	1	1
						SED7AVVYCAR	2	0.9333	1
Q5534-1	P01766	HV305_HUMAN		lg heavy chain V-III region BRO	0.9989	9.17	1	1	2
Q5534-2	P01767	HV306_HUMAN		lg heavy chain V-III region BUT	0.9989	9.57	1	1	2
Q5534-3	P01763	HV302_HUMAN		lg heavy chain V-III region WEA	0.9989	9.65	1	1	2
						AED7AVVYCAR	2	0.9982	2
Q5535-1	P06331	HV209_HUMAN		lg heavy chain V-II region ARH-77	0.9666	10.96	1	1	2
Q5535-2	P01825	HV207_HUMAN		lg heavy chain V-II region NEWM	0.9666	13.68	1	1	2
						LSSVTAAD7AVVYCAR	2	0.9666	2
Q5536-1	P01834	IGKC_HUMAN	IGKC	lg kappa chain C region	1.0000	83.96	21	25	104
						AAPSVFIFFPPSDEQLK	2	0.9465	3
						ACEVTHQGLSSPVTK	2	0.9949	3
						CEVTHQGLSSPVTK	2	0.9972	3
						DSTYLSLSTLTLSK	2	0.9997	5
						EVTHQGLSSPVTK	2	0.9962	2
						HKVYACEVTHQGLSSPVTK	3	0.9993	4
						KVDNALQSGNSQESVTEQDSK	3	0.9436	1
						SGTASVCLLNIFYPR	2	0.9997	10
						SGTASVCLLNIFYPR	3	0.9996	4
						SGTASVCLLNIFYPRE	2	0.9872	4
						SLSTLTLSK	2	0.9662	1
						STYLSLSTLTLSK	2	0.947	2
						TVAAPSVFIFFPPSDEQLK	2	0.9997	20
						TVAAPSVFIFFPPSDEQLK	3	0.9992	15
						VCLLNIFYPR	2	0.8451	2
						VDNALQSGNSQESVTE	2	0.9882	2
						VDNALQSGNSQESVTEQDSK	2	0.9997	4
						VDNALQSGNSQESVTEQDSK	3	0.9989	2
						VDNALQSGNSQESVTEQDSKSTYLSLSTLTLSK	3	0.9992	5
						VFIFFPPSDEQLK	2	0.9189	4
						VYACEVTHQGL	2	0.9902	1
						VYACEVTHQGLSSPVT	2	0.9455	1
						VYACEVTHQGLSSPVT	2	0.9881	2
						VYACEVTHQGLSSPVT	2	0.9997	3
						VYACEVTHQGLSSPVT	3	0.9996	1
Q5537-1	P01857	IGHG1_HUMAN	IGHG1	lg gamma-1 chain C region	1.0000	38.18	15	17	35
						DYFPEPV	2	0.9023	1
						DYFPEPVT	2	0.938	1
						DYFPEPVTYSWNSGALTSVHTFP	2	0.9804	1
						FNWYVDGVEVHNAK	2	0.9997	2
						FNWYVDGVEVHNAK	3	0.9971	1
						GPSVFPLAPSK	2	0.9996	3
						NQVSLTCLVK	2	0.9995	3
						NWYVDGVEVHNAK	2	0.9912	3
						STSGTAAALGCLVK	2	0.9996	2
						TPEVTCVVVDVSH	2	0.9846	3
						TPEVTCVVVDVSH	2	0.8276	2
						TPEVTCVVVDVSHDEPEVK	2	0.9996	3
						TPEVTCVVVDVSHDEPEVK	3	0.9997	5
						TTPPVLDSDGFFLY	2	0.9788	1
						TTPPVLDSDGFFLYSK	3	0.998	2
						VVSVLTVLHQDWLNGK	3	0.9558	1
						WYVDGVEVHNAK	2	0.9784	1
Q5538-1	P01859	IGHG2_HUMAN	IGHG2	lg gamma-2 chain C region	1.0000	37.12	14	15	31
						CCVECPPCAPPVAGPS	2	0.8399	1
						DYFPEPV	2	0.9023	1
						DYFPEPVT	2	0.938	1
						DYFPEPVTYSWNSGALTSVHTFP	2	0.9804	1
						FNWYVDGVEVHNAK	2	0.9997	2
						GPSVFPLAPCSR	2	0.9996	3
						NQVSLTCLVK	2	0.9995	3
						NWYVDGVEVHNAK	2	0.9912	3
						STSESTAALGCLVK	2	0.9996	5
						STSESTAALGCLVK	3	0.9764	2
						TPEVTCVVVDVSH	2	0.9846	3
						TPEVTCVVVDVSH	2	0.8276	2
						TPEVTCVVVDVSHDEPEVQF	2	0.975	2
						VVSVLTVVHQD	2	0.8156	1
						WYVDGVEVHNAK	2	0.9784	1
Q5539-1	P01860	IGHG3_HUMAN	IGHG3	lg gamma-3 chain C region	1.0000	12.2	5	5	12
						GPSVFPLAPCSR	2	0.9996	3
						STSGTAAALGCLVK	2	0.9996	2
						TPEVTCVVVDVSH	2	0.9846	3
						TPEVTCVVVDVSH	2	0.8276	2
						TPEVTCVVVDVSHDEPEVQF	2	0.975	2
Q5540-1	P01861	IGHG4_HUMAN	IGHG4	lg gamma-4 chain C region	1.0000	24.77	6	6	15
						FNWYVDGVEVHNAK	2	0.9997	2
						GPSVFPLAPCSR	2	0.9996	3
						NQVSLTCLVK	2	0.9995	3
						STSESTAALGCLVK	2	0.9996	5
						TTPPVLDSDGFFLY	2	0.9788	1
						VVSVLTVLHQDWLNGK	3	0.9558	1
Q5541-1	P01876	IGHA1_HUMAN	IGHA1	lg alpha-1 chain C region	1.0000	17.85	5	5	9
						DASGVITFTTWPSSGK	2	0.9997	4
						QEPSGQTTTFAVTSILR	2	0.9972	1
						TFCTCTAAYPESK	2	0.9991	2
						TPLTATLSK	2	0.9982	1
						WLQGSQELPR	2	0.9443	1
Q5542-1	P02042	HBD_HUMAN	HBD	Hemoglobin subunit delta	1.0000	92.52	60	78	235
						AFSDGLAHLNLK	2	0.9924	5
						AGVANALAHKYH	2	0.9134	1
						DKLHVDPENFR	2	0.9673	3
						DKLHVDPENFR	3	0.9414	2
						EFTPCIMQAAVQK	2	0.963	2
						FFESFGDLS	2	0.939	1
						FFESFGDLSPPDAVMGNPK	2	0.9997	3
						FSDGLAHLNLK	2	0.9345	3
						FSDGLAHLNLK	3	0.8507	1
						GAFSGLAHLNLK	2	0.9951	6
						GLAHLNLK	2	0.9422	1
						GNVLVCVLAR	2	0.9268	2
						GTFSQLSELHCDK	2	0.9894	1
						GTFSQLSELHCDKLHVDPENFR	3	0.9938	2
						HCDKLHVDPENFR	2	0.9801	2
						HCDKLHVDPENFR	3	0.8269	1
						HLTPEEK	2	0.9103	2
						HVDPENFR	2	0.9515	1
						KLHVDPENFR	2	0.9703	1
						KLHVDPENFR	3	0.8815	1
						KVLGAFSD	2	0.8856	1
						KVLGAFSDGLAHLN	2	0.961	2
						KVLGAFSDGLAHLN	2	0.9751	3
						KVLGAFSDGLAHLNL	2	0.9889	2
						KVLGAFSDGLAHLNLK	2	0.9997	6
						KVLGAFSDGLAHLNLK	3	0.9997	12
						KVLGAFSDGLAHLNLK	4	0.9375	1
						LAHLNLK	2	0.8465	1
						LHCDKLHVDPENFR	2	0.9735	2
						LHCDKLHVDPENFR	3	0.8133	1
						LHVDPENFR	2	0.9997	7
						LHVDPENFR	3	0.9996	4
						LLGNLVLC	2	0.9772	1
						LLGNLVLCV	2	0.9694	2

						LLGNVLVCVL	2	0.9978	2
						LLGNVLVCVLA	2	0.9959	2
						LLGNVLVCVLAR	2	0.9997	7
						LLGNVLVCVLAR	3	0.9996	2
						LLVVPW	2	0.9962	2
						LLVVPWT	2	0.9952	3
						LLVVPWTD	2	0.9963	2
						LLVVPWTD	3	0.9994	5
						LSELHCDKLHVDPENFR	2	0.9902	3
						LSELHCDKLHVDPENFR	3	0.9641	1
						LVVYPWTQR	2	0.996	3
						RLVVYPWTQR	2	0.9957	4
						RLVVYPWTQR	3	0.9801	2
						SDGLAHLNKL	2	0.9895	5
						SDGLAHLNKL	3	0.8253	1
						SELHCDKLHVDPENFR	2	0.9888	3
						SELHCDKLHVDPENFR	3	0.8897	1
						SELHCDKLHVDPENFR	4	0.9011	1
						SQSELHCDKLHVDPENFR	3	0.9564	1
						TAVNALWGK	2	0.9997	2
						VAGVANALAHK	2	0.9934	2
						VAGVANALAHKYH	2	0.9256	1
						VDPENFR	2	0.94	1
						VGGEALGR	2	0.9882	2
						VHLPTEK	2	0.9997	11
						VLGAFSDGLAH	2	0.8917	1
						VLGAFSDGLAHL	2	0.9865	6
						VLGAFSDGLAHL	2	0.992	4
						VLGAFSDGLAHLN	2	0.9941	4
						VLGAFSDGLAHLN	2	0.9966	8
						VLGAFSDGLAHLN	2	0.9998	18
						VLGAFSDGLAHLN	3	0.9997	13
						VLGAFSDGLAHLN	2	0.9329	2
						VNVDVGGGEALGR	2	0.9997	6
						VNVDVGGGEALGR	2	0.9716	2
						VVAGVANALA	2	0.8581	1
						VVAGVANALAH	2	0.9932	2
						VVAGVANALAHK	2	0.9997	3
						VVAGVANALAHK	3	0.9993	1
						VVAGVANALAHKY	2	0.9757	2
						VVAGVANALAHKYH	2	0.9996	3
						VVAGVANALAHKYH	3	0.9919	1
						VVAGVANALAHKYH	4	0.9959	1
						VVYPWTQR	2	0.9788	2
Q5543-1	P02100	HBE_HUMAN	HBE1	Hemoglobin subunit epsilon	1.0000	10.2	1	0.9348	1
						LSELHCDKLHVDPEN	2	0.9348	1
Q5544-1	P02533	K1C14_HUMAN	KRT14	Keratin, type I cytoskeletal 14	1.0000	54.24	22	27	49
						ADLEMQIESLKEELAYLK	3	0.9948	3
						ADLEMQIESLKEELAYLKK	3	0.9862	2
						ALEANADLEVK	2	0.9994	2
						APSTYGGGLSVSSSR	2	0.9995	2
						ASLENSLEETK	2	0.9996	1
						ASLENSLEETKGR	2	0.9933	1
						CEMEQQNQEVK	2	0.9997	2
						DAEEWFFTK	2	0.9989	2
						DAEEWFFTKTEELNR	2	0.9987	3
						DAEEWFFTKTEELNR	3	0.9614	1
						EVATNSELVQSGK	2	0.9997	2
						GSCGIGGGGGGSSSR	2	0.9993	1
						ILNEMRDQYEK	2	0.9902	1
						ILTATVDNANVLLQIDNAR	2	0.9995	2
						ILTATVDNANVLLQIDNAR	3	0.9973	3
						ISSVLGGGSCR	2	0.9994	1
						LLEGEDAHLSQQSSGSSQSSR	3	0.9995	3
						MSVEADINGLR	2	0.9994	1
						NHEEEMNALR	2	0.9996	2
						RILEGEDAHLSQQSSGSSQSSR	3	0.9985	3
						TKYTEELNR	2	0.9934	1
						TKYTEELNR	3	0.821	1
						TMQNLEIELQSLSMK	2	0.9986	3
						TMQNLEIELQSLSMK	3	0.9023	2
						VTMQNLNDR	2	0.9989	1
						YCMQLAQIQEMIGSVEEQLAQLR	2	0.9986	1
						YCMQLAQIQEMIGSVEEQLAQLR	3	0.9981	2
Q5545-1	P02538	K2C6A_HUMAN	KRT6A	Keratin, type II cytoskeletal 6A	1.0000	37.77	17	17	33
						ADTLTDEINFLR	2	0.9995	3
						AIGGGLSSVGGGSSTIK	2	0.9995	2
						ALYDAELSQQMTHISDTSVVLMDNNR	3	0.9992	3
						DVDAAYMNKVELQAK	2	0.9988	2
						EYQELMNVK	2	0.9948	1
						GSGGLGGACGGAGGFSR	2	0.9984	2
						ISHGSGGACGGAGGFSR	2	0.9994	2
						LLKEYQELMNVK	2	0.9981	3
						NKLEGLDALQK	3	0.9118	1
						OCANLQAIAADAEQR	2	0.9973	2
						QNLEPLFEQYNNLR	2	0.9977	3
						RQLDSIVGER	2	0.9846	1
						SRAEAESWYQTK	2	0.9945	2
						SRAEAESWYQTKYEELQVTAGR	3	0.9983	2
						TAAENEFVTLKK	2	0.9973	1
						WTLLEQGTGK	2	0.9985	1
						YEELQVTAGR	2	0.9991	2
Q5546-1	P02545-6	LMNA_HUMAN	LMNA	Isoform 6 of Prelamin-A/C	1.0000	15.15	9	9	10
Q5546-2	P02545-2	LMNA_HUMAN	LMNA	Isoform C of Prelamin-A/C	1.0000	16.26	9	9	10
						AAYEAELGDAR	2	0.9995	1
						EAAIATLSEKR	2	0.9838	1
						EGOLIAAQR	2	0.9861	1
						ITESEEVVSR	2	0.9994	1
						LADALQELR	2	0.9986	1
						LAVYIDR	2	0.9977	1
						SGAQASSTPLSPTR	2	0.991	1
						SLETENAGLR	2	0.9971	1
						TLEGELHDLR	2	0.9897	2
Q5547-1	P02545-3	LMNA_HUMAN	LMNA	Isoform ADelta10 of Prelamin-A/C	1.0000	18.93	10	10	11
Q5547-2	P02545	LMNA_HUMAN	LMNA	Prelamin-A/C	1.0000	18.07	10	10	11
						AAYEAELGDAR	2	0.9995	1
						ASASGSGAGVGPISGSSASSVTVTR	2	0.9159	1
						EAAIATLSEKR	2	0.9838	1
						EGOLIAAQR	2	0.9861	1
						ITESEEVVSR	2	0.9994	1
						LADALQELR	2	0.9986	1
						LAVYIDR	2	0.9977	1
						SGAQASSTPLSPTR	2	0.991	1
						SLETENAGLR	2	0.9971	1
						TLEGELHDLR	2	0.9897	2
Q5548-1	P02647	APOA1_HUMAN	APOA1	Apolipoprotein A-I	1.0000	68.91	27	32	85
						AKPALEDLR	2	0.9982	1
						ATEHLSTSEK	2	0.9997	3
						ATEHLSTSEK	3	0.9958	1
						DLATVYVDVILKDSGR	2	0.9997	3
						DLATVYVDVILKDSGR	2	0.9995	6
						DLATVYVDVILKDSGRDYVSQFEGSALGK	3	0.999	6
						DSGRDYVSQFEGSALGK	2	0.9994	2

						DSGRDVSQFEGSALGK	3	0.9977	2
						DVVSQFEGSALGK	2	0.9997	3
						EQLGPVTQEFWDNLEK	2	0.9997	5
						EQLGPVTQEFWDNLEKETGLR	3	0.9256	1
						EQLGPVTQEFWDNLEKETGLRQEMSK	3	0.9019	1
						LEALKENGGAR	2	0.9992	2
						LIDNWDISTTSFK	2	0.9997	8
						LRIQLGPVTQEFWDNLEK	3	0.9889	4
						LREQLGPVTQEFWDNLEKETGLR	3	0.9976	2
						LREQLGPVTQEFWDNLEKETGLR	4	0.9899	1
						LSPLGEEMR	2	0.9921	1
						QGLLPVLESF	2	0.9692	2
						QGLLPVLESFK	2	0.9997	3
						QGLLPVLESFKVSLSALEEYTK	3	0.983	2
						QKVEPLRAELQEGAR	2	0.9343	3
						SLSALEEYTK	2	0.9578	1
						THLAPYSDELRL	2	0.9997	4
						THLAPYSDELRL	3	0.9996	1
						THLAPYSDELRLQ	2	0.983	2
						VKQLATVYVDVLK	2	0.9889	4
						VQPYLDDFOKK	2	0.9969	1
						VSLSALEEYTK	2	0.9997	4
						VSLSALEEYTKK	2	0.9993	2
						VSLSALEEYTKK	3	0.9847	2
						WQEMEELR	2	0.9946	2
Q5549-1	P02649	APOE_HUMAN	APOE	Apolipoprotein E	1.0000	65.93	20	22	42
						AATVGSAGPLQER	2	0.9996	3
						AKLEEQAQIR	2	0.9993	4
						AYKSELEQLTPVAEETR	2	0.999	1
						AYKSELEQLTPVAEETR	3	0.9653	2
						DRLDEVKEQVAEVR	2	0.9971	2
						DRLDEVKEQVAEVR	3	0.9956	2
						GEVQAMLGQSTELR	2	0.9974	2
						KVEQAVETPEPELR	2	0.9929	2
						LAVYQAGAR	2	0.9993	1
						LDEVKEQVAEVR	2	0.9986	1
						LEEQAQIR	2	0.9924	2
						LGADMEDVCGR	2	0.9991	1
						LGPLVEQGR	2	0.9995	1
						LKSWFEPLVEDMQR	3	0.9981	2
						LQAEAFQAR	2	0.9993	1
						LSKELQAAQAR	2	0.9607	1
						QQTWQSGQR	2	0.9897	1
						QWAGLVEK	2	0.9229	1
						SELEQLTPVAEETR	2	0.9997	2
						SWFEPLVEDMQR	2	0.9997	2
						VQAAVGTSAAPVPSDNH	2	0.9997	4
						WYQTLSEQVQELLSSQVQELR	3	0.9995	4
Q5550-1	P02652	APOA2_HUMAN	APOA2	Apolipoprotein A-II	1.0000	69	7	9	22
Q5550-2	V9GYM3	V9GYM3_HUMAN	APOA2	Apolipoprotein A-II	1.0000	51.88	7	9	22
						AGTELNVNLSYFVELGTQPATQ	3	0.9994	3
						EPCVESLSVQYFQTVTDYGK	2	0.9997	5
						EPCVESLSVQYFQTVTDYGK	3	0.9981	3
						EPCVESLSVQYFQTVTDYGKDLMEK	3	0.9769	2
						SKQLTPLIK	2	0.9958	1
						SKQLTPLIKK	2	0.9656	1
						SPLQAEAK	2	0.9997	1
						VKSPQLQAEAK	2	0.9994	4
						VKSPQLQAEAK	3	0.9979	2
Q5551-1	P02671	FIBA_HUMAN	FGA	Fibrinogen alpha chain	1.0000	42.84	38	48	153
						ADSGEGDFAEGGGVR	2	0.9928	2
						AQLVDMK	2	0.9993	1
						DCDDVLQTHPSG	2	0.9915	1
						DCDDVLQTHPSGTQ	2	0.9097	2
						DCDDVLQTHPSGTQSGIFNIK	2	0.9997	2
						DCDDVLQTHPSGTQSGIFNIK	3	0.9991	4
						DCDDVLQTHPSGTQSGIFNIKPGSSK	3	0.9993	3
						DQETSLGGWLIQQR	2	0.9374	1
						DSDWPFCSDEDWNYK	2	0.9997	4
						DSHSLTNIMELR	3	0.9706	1
						EVLDKDYEDQK	2	0.9915	2
						EVVTSEDGSDCEAMDGLTSLGIGTLDGFR	3	0.9699	1
						GADYSLR	2	0.9939	1
						GFGLNDEGEFEWLGNDYLHLLTQR	3	0.9997	16
						GGSTVGTGSETESPR	2	0.9997	4
						GLIDEVNQDFTNR	2	0.9998	10
						GLIDEVNQDFTNR	3	0.9997	3
						GLIDEVNQDFTNRINK	2	0.9984	2
						GSESGFTNTK	2	0.9992	1
						GSLRVLEEDWAGNEAYAEYHFR	3	0.9993	4
						GSLRVLEEDWAGNEAYAEYHFR	4	0.8614	1
						HQSACKSDSWPFCSDWNYK	3	0.9094	3
						HRHPDEAAFDFASTGK	3	0.9956	4
						IFSVCYCDQETSLGGWLIQQR	2	0.9997	5
						IFSVCYCDQETSLGGWLIQQR	3	0.9996	12
						IRPLVTQ	2	0.9997	2
						LEVVDIK	2	0.9994	4
						MELERPGNEITR	2	0.9974	2
						MKGLIDEVNQDF	2	0.9055	2
						MKGLIDEVNQDFTNR	2	0.9994	2
						MKGLIDEVNQDFTNR	3	0.9992	2
						NNSPYEINGVVVVSFR	2	0.9998	11
						NNSPYEINGVVVVSFR	3	0.9993	4
						NSLFEYQK	2	0.9943	2
						PFCSDWNYK	2	0.9608	2
						QLEQVIK	2	0.9107	1
						RGFGLNDEGEFEWLGNDYLHLLTQR	3	0.9996	4
						RGFGLNDEGEFEWLGNDYLHLLTQR	4	0.9987	3
						RLEVDIK	2	0.9986	1
						RLEVDIK	3	0.9963	1
						SPYEINGVVVVSFR	2	0.8368	1
						TFPGFSPMLGEFVSETSR	2	0.9982	3
						VELEDWAGNEAYAEYHFR	2	0.9997	3
						VELEDWAGNEAYAEYHFR	3	0.9997	7
						VGSEAEYALQVS	2	0.9711	1
						VQHILQLQK	2	0.995	1
						VQHILQLQK	3	0.9148	1
						WPFCSDEDWNYK	2	0.9931	3
Q5552-1	P02675	FIBB_HUMAN	FBG	Fibrinogen beta chain	1.0000	68.43	56	64	149
						AHYGGFTVQNEANK	2	0.9997	3
						AHYGGFTVQNEANKY	2	0.9869	1
						AHYGGFTVQNEANKYQISVKN	2	0.9995	2
						AHYGGFTVQNEANKYQISVKN	3	0.9993	2
						APDAGGCLHAD	2	0.8727	1
						APDAGGCLHADPDGLVCLPTGCOLQEQALLQQRPI	3	0.9924	3
						APDAGGCLHADPDGLVCLPTGCOLQEQALLQQRPI	3	0.9556	2
						APDAGGCLHADPDGLVCLPTGCOLQEQALLQQRPIR	4	0.999	4
						DETVNSNIPTNLR	2	0.8911	1
						DMNTENGSGWTVCINR	2	0.9944	2
						DNENNVNYSSELEK	2	0.9997	3
						ECCEIRK	2	0.9964	1
						ECCEIRK	2	0.9899	1
						EDGGGWYNNR	2	0.9992	4

							EEAPSLRPAPPISGGGYR		3	0.99	1
							GGTSEMRLQIPSSVKNPR		3	0.9992	2
							HGTDDGVVMNNWK		2	0.9993	4
							HGTDDGVVMNNWK		3	0.9751	3
							HQLYIDETVNSIPTNLR		2	0.9997	1
							HQLYIDETVNSIPTNLR		3	0.9992	2
							IDETVNSIPTNLR		2	0.9815	3
							IQKLESVSAQMEYCR		2	0.9996	2
							IQKLESVSAQMEYCR		3	0.985	1
							IRPFFPQ		2	0.9798	2
							IRPFFPQQ		2	0.9994	3
							KAPDAGGCLHADPD		2	0.9223	1
							KAPDAGGCLHADPDGLVCLPTGCQLQE		3	0.9861	4
							KAPDAGGCLHADPDGLVCLPTGCQLQEA		3	0.8183	2
							KAPDAGGCLHADPDGLVCLPTGCQLQEA		3	0.9823	3
							KAPDAGGCLHADPDGLVCLPTGCQLQEA		3	0.8677	1
							KAPDAGGCLHADPDGLVCLPTGCQLQEA		3	0.9916	3
							KAPDAGGCLHADPDGLVCLPTGCQLQEA		3	0.9532	1
							KAPDAGGCLHADPDGLVCLPTGCQLQEA		4	0.9993	7
							KGGETSEMYLIQPDSSVKPYR		3	0.9996	5
							KGGETSEMYLIQPDSSVKPYR		4	0.9977	1
							KREEAPSLRPAPPISGGGYR		3	0.988	1
							KWDOPYQGFNVATNTDGG		3	0.972	1
							LESVSAQMEYCR		2	0.9997	3
							MGPTLLIEMEDWK		2	0.9997	6
							MGPTLLIEMEDWK		3	0.9994	2
							NSVDELNNVEA		2	0.9283	1
							NSVDELNNVEAVSQTS		2	0.9765	2
							NSVDELNNVEAVSQTS		2	0.9929	1
							NSVDELNNVEAVSQTS		2	0.9809	1
							NSVDELNNVEAVSQTS		3	0.9996	4
							NYCGLPGEYWLGNDK		2	0.9996	4
							NYCGLPGEYWLGNDKISQLTR		2	0.9979	1
							NYCGLPGEYWLGNDKISQLTR		3	0.9971	1
							QDGSVDFGR		2	0.9056	1
							QGFNVATNTDGG		2	0.9997	3
							QLYIDETVNSIPTNLR		2	0.9851	1
							QVKDNNVNVYSLEK		3	0.8346	1
							REEAPSLRPAPPISGGGYR		3	0.9993	3
							SILENLR		2	0.9991	2
							SIQKLESVSAQMEYCR		3	0.9992	3
							TPCTVSCNIPVVGK		2	0.9997	7
							TPCTVSCNIPVVGKECEIIR		3	0.9993	3
							TPCTVSCNIPVVGKECEIIRK		3	0.8241	1
							TVSCNIPVVGK		2	0.9488	1
							VYCDMNTENGWTVIQNR		2	0.9997	5
							VYCDMNTENGWTVIQNR		3	0.9925	2
							YIDETVNSIPTNLR		2	0.8772	1
							YQISVKN		2	0.9975	1
							YWGGQYTWOMAK		2	0.9997	4
Q553-1	P02679	FIBG_HUMAN	FGG	Fibrinogen gamma chain	1.0000		54.08		47	53	120
Q553-2	P02679-2	FIBG_HUMAN	FGG	Isoform Gamma-A of Fibrinogen gamma chain	1.0000		56.06		47	53	120
							AIQLTNPDESSKP		2	0.936	1
							AIQLTNPDESSKPMMDAATLK		3	0.9968	2
							ALRVELEDWNGR		3	0.9007	1
							ASILTHDSSIR		2	0.9082	1
							ASTPNGVDNGIWWATWK		2	0.9971	4
							CHAGHLNGVYVQGTYSK		3	0.9979	3
							DNCILDER		2	0.9997	5
							DTVQIHDTGK		2	0.999	1
							EASILTHDSSIR		2	0.843	1
							EGFGHLSPTGTTEFWLGNEK		2	0.9997	4
							EGFGHLSPTGTTEFWLGNEK		3	0.9996	4
							FGSYCPTTCGIADFL		2	0.9461	2
							FGSYCPTTCGIADFLSTY		2	0.9962	2
							FGSYCPTTCGIADFLSTYQ		2	0.9834	2
							FGSYCPTTCGIADFLSTYQT		2	0.9978	2
							FGSYCPTTCGIADFLSTYQTK		7	0.9998	7
							FGSYCPTTCGIADFLSTYQTK		3	0.9996	4
							FGSYCPTTCGIADFLSTYQTKV		2	0.9937	2
							GIADFLSTYQTK		2	0.9958	2
							IHLISTQ		2	0.976	1
							IHLISTQSAIPYALR		2	0.9997	4
							IHLISTQSAIPYALR		3	0.9995	2
							IHLISTQSAIPYALRV		2	0.9677	1
							IHLISTQSAIPYALRVELEDWNGR		3	0.997	5
							KEFGHLSPTGTTEFWLGNEK		3	0.9592	2
							KMLEIMKYEASILTHDSSIR		3	0.9918	2
							LDGSSVDFK		2	0.9988	4
							LDGSSVDFK		2	0.9991	2
							LQEIYNSNNQK		2	0.9914	1
							LSPTGTTEFWLGNEK		2	0.9199	1
							LTIGEGQQHHLGGAK		2	0.9994	2
							MLEIMKYEASILTHDSSIR		3	0.9988	3
							OSGLYFIKPLK		2	0.9997	2
							OSGLYFIKPLK		3	0.9664	1
							RLDGSVDFK		2	0.9992	2
							RVELEDWNGR		2	0.9422	1
							RYLQEIYNSNNQK		2	0.8573	1
							SILTHDSSIR		2	0.9949	4
							SPTGTTEFWLGNEK		2	0.9861	3
							STQSAIPYALR		2	0.9526	1
							TGTTTEFWLGNEK		2	0.9087	1
							TSTADYAMFK		2	0.9992	1
							VAQLEAQCEPCK		2	0.9997	2
							VAQLEAQCEPCKD		2	0.9969	2
							VAQLEAQCEPCKD		2	0.9829	2
							VAQLEAQCEPCKD		2	0.9977	2
							VAQLEAQCEPCKDTVQIHDTGK		3	0.9987	3
							VAQLEAQCEPCKDTVQIHDTGKDCQDIANK		3	0.9982	1
							VAQLEAQCEPCKDTVQIHDTGKDCQDIANK		4	0.8362	1
							VELEDWNGR		2	0.9996	2
							YEASILTHDSSIR		2	0.9997	4
							YEASILTHDSSIR		3	0.9956	1
							YLQEIYNSNNQK		2	0.9997	3
Q554-1	P02730	B3AT_HUMAN	SLC4A1	Band 3 anion transport protein	1.0000		6.48		5	6	14
							AAATLMSER		2	0.9638	1
							ADFLQPVGLFVR		2	0.9996	2
							FLFVLGPEAPHIDYTLGLR		3	0.9996	3
							LQEAALAEAVELPVPIR		2	0.9997	4
							LQEAALAEAVELPVPIR		3	0.9914	1
							LQEAALAEAVELPVPIRF		2	0.9938	3
Q555-1	P02743	SAMP_HUMAN	APCS	Serum amyloid P-component	1.0000		40.36		9	9	16
							AYSLSFSYNTGGR		2	0.9996	3
							DNELLVYK		2	0.9988	1
							DNELLVYKER		2	0.964	1
							GYVIKPLVWV		2	0.9997	4
							IVGLQEQDSYGGGKDFDR		2	0.9994	2
							NILDWQALNWEIR		2	0.8979	1
							OGTYVEAQPK		2	0.9965	1
							RAYSDLSR		2	0.9379	1
							VGEYSLYIGR		2	0.9997	2
Q556-1	P02745	C1QA_HUMAN	C1QA	Complement C1q subcomponent subunit A	0.9997		13.47		3	3	4

						GHYQGSEADSVFSGFLIFPSA	2	0.8959	2
						KGHYQGSEADSVFSGFLIFPSA	3	0.9476	1
						SLGFCDTTNK	2	0.997	1
Q5557-1	P02747	C1QC_HUMAN	C1QC	Complement C1q subcomponent subunit C	0.9239	4.08	1	1	1
						VVTFGHTSK	2	0.9239	1
Q5558-1	P02748	C09_HUMAN	C9	Complement component C9	1.0000	33.63	16	19	38
						AIEDYHNEFSVR	2	0.9997	3
						CLCACPFKFEIGACEISK	2	0.9775	1
						CLCACPFKFEIGACEISK	3	0.9898	1
						DRDGNLTYYR	2	0.985	1
						DRVVESELAR	2	0.9904	2
						DVLTTFVDDIK	2	0.9994	4
						GEYFALETYGTTHY	2	0.963	2
						GTVIDVDFVNWASSINDAPVLISQK	3	0.9697	1
						ISEGLPALEFPNE	2	0.8931	1
						KYAFELK	2	0.9856	1
						LSPIYNLVPVK	2	0.9882	2
						NFRTEHYEEQIEAFK	3	0.9893	2
						RPWNVASLIVETK	2	0.9994	4
						RPWNVASLIVETK	3	0.9994	3
						SENLDVVSILR	2	0.9656	2
						TEHYEQIEAFK	2	0.9997	3
						TEHYEQIEAFK	3	0.9868	2
						TSNFNAISLK	2	0.9997	2
						VVESELAR	2	0.9894	1
Q5559-1	Q5VY30	Q5VY30_HUMAN	BBP4	Retinol binding protein 4, plasma, isoform CRA_b	1.0000	20.1	4	4	9
Q5559-2	P02753	RET4_HUMAN	BBP4	Retinol-binding protein 4	1.0000	19.9	4	4	9
						LIVHNGYCDGR	2	0.9885	1
						LLNLDTGTCADSYSFVFSR	2	0.9996	5
						LLNLDTGTCADSYSFVFSR	2	0.9916	1
						YWGVSFLQK	2	0.9883	2
Q5560-1	P02760	AMBP_HUMAN	AMBP	Protein AMBP	1.0000	35.23	13	15	34
						AFQLWAFDAVK	2	0.9996	3
						ETLLQDFR	2	0.9997	2
						GECVPGGEPEPIPIR	2	0.9997	2
						GVCETSGAYEK	2	0.9997	1
						GVCETSGAYEKTDTDGK	2	0.9997	3
						KGVCETSGAYEK	2	0.9997	4
						KGVCETSGAYEKTDGK	2	0.999	1
						KGVCETSGAYEKTDGK	3	0.9973	3
						MTVSTLVLGEGATEAISMSTR	2	0.9997	3
						TVAACNLPIVR	2	0.9917	2
						VLGEGATEAISMSTR	2	0.9938	1
						VVAQGVGVPDSIFMTADRGECVPGGEPEPIPIR	3	0.9871	2
						WYNLAIGSTCPWLK	2	0.9897	4
						WYNLAIGSTCPWLK	3	0.9278	1
						WYNLAIGSTCPWLK	2	0.996	2
Q5561-1	P02763	A1AG1_HUMAN	ORM1	Alpha-1-acid glycoprotein 1	1.0000	19.4	4	4	8
						EQLGFEYALDCLR	2	0.9995	4
						SDVVYTDWK	2	0.9954	2
						SDVVYTDWK	2	0.9671	1
Q5562-1	P02766	TTHY_HUMAN	TTR	Transthyretin	1.0000	53.74	2	5	9
						YVGGQEHAFLIUR	2	0.9987	1
						AADDTWEPFASGK	2	0.9995	1
						GSPAINVAHVFR	2	0.9821	2
						KAADDTWEPFASGK	2	0.964	1
						RYTIALSPISSTIAVATNKE	3	0.9881	2
						TSESGELHGLTTEEFVEVGIKVEIDTK	3	0.9978	3
Q5563-1	P02768	ALBU_HUMAN	ALB	Serum albumin	1.0000	70.28	61	74	149
						AACLKP	2	0.9888	1
						AAFTCCQAADK	2	0.9996	1
						ADDKETCFAEKG	2	0.9987	3
						ADDKETCFAEKGK	2	0.9995	6
						ADDKETCFAEKGK	3	0.9983	2
						AFAGYLLQCCPFEDHVK	3	0.9005	1
						ALVLIAFAQYLLQCCPFEDHVK	2	0.9997	5
						ALVLIAFAQYLLQCCPFEDHVK	3	0.9997	11
						ALVLIAFAQYLLQCCPFEDHVK	4	0.999	2
						AYLLQCCPFEDHVK	2	0.9911	4
						ADYLQCCPFEDHVK	3	0.9074	1
						AVMDFAAFVEK	2	0.9998	1
						AVMDFAAFVEK	3	0.9938	1
						CAAADPHECYA	2	0.9868	2
						CAAADPHECYA	2	0.8159	1
						CAAADPHECYA	3	0.9913	1
						CTESLVNR	2	0.9973	1
						CTESLVNR	2	0.8874	1
						DLGEENFK	2	0.9792	1
						DVCKNYAEAK	2	0.8516	1
						DVFLGMFLYER	2	0.9997	5
						ECCEKPLEK	2	0.9258	1
						EFNAETTFHADICTLSEK	2	0.9893	1
						EFNAETTFHADICTLSEK	3	0.9753	1
						FKDLGEENFK	2	0.988	1
						FKDLGEENFK	3	0.9581	1
						FQNALLVR	2	0.9986	1
						FSALEVDETVVPK	2	0.8615	1
						FYAPELLFAK	2	0.9695	2
						HPYFYAPELLFAK	2	0.9785	2
						HPYFYAPELLFAK	3	0.9988	4
						KLVAASQAALGL	2	0.992	1
						KQTALVELVK	2	0.956	1
						KQTALVELVK	3	0.9953	1
						KVPQVSTPLVEV	2	0.9522	1
						KVPQVSTPLVEVSR	3	0.9997	2
						KYLYEAR	2	0.8126	1
						LCTVATLR	2	0.9964	1
						LDELDEGK	2	0.9476	1
						LKECKEPLLEK	3	0.9097	1
						LVAASQAALGL	2	0.9991	3
						LVNEVTEFAK	2	0.9997	3
						LVRPEVDVMCTAFHDNEETFLK	3	0.8761	1
						LVTDLTK	2	0.9647	1
						MPCAEDYLSVNLQCLVLEK	3	0.9986	2
						QNCLEFQGLGEYK	2	0.9997	3
						QNCLEFQGLGEYKFNQALLVR	3	0.9976	2
						QTAALVELK	2	0.9727	1
						QYLLQCCPFEDHVK	2	0.9814	1
						RHPDYSVLLLR	2	0.9993	4
						RHPDYSVLLLR	3	0.9996	5
						RHPYFYAPELLFAK	2	0.9984	2
						RHPYFYAPELLFAK	4	0.9961	2
						RMPCAEDYLSVNLQCLVLEK	3	0.9858	2
						RPCFSAL	2	0.9674	1
						RPCFSALEVDETVVPK	2	0.9984	3
						RPCFSALEVDETVVPK	3	0.9996	2
						SHCIAEVENDEMPADPLSLAADFVESK	3	0.9993	3
						SLHTLFGDK	2	0.999	1
						SLHTLFGDKLCTVAT	2	0.8361	1
						SLHTLFGDKLCTVATLR	2	0.9995	3
						SLHTLFGDKLCTVATLR	3	0.9994	1
						TCVADESAENCDK	2	0.9997	3
						TCVADESAENCDKSLHTLFGDK	3	0.9489	1

						VFDEFKPL	2	0.8356	1
						VFDEFKPLVEEPQ	2	0.8081	1
						VFDEFKPLVEEPQN	2	0.8802	1
						VFDEFKPLVEEPQNL	2	0.9592	2
						VFDEFKPLVEEPQNLK	2	0.9997	4
						VFDEFKPLVEEPQNLK	3	0.9997	3
						VHTECGHGLLECAADR	3	0.9991	2
						VHTECGHGLLECAADRDLAK	3	0.9047	1
						VPOVSTPTLVEYSR	2	0.9993	3
						YLVEIAR	2	0.9981	1
Q5564-1	P02787	TRFE_HUMAN	TF	Serotransferrin	1.0000	31.23	23	26	58
						CDEWSNVSGK	2	0.9952	1
						CLVEKGDVAFVK	2	0.9692	2
						CSTSSLEACTFR	2	0.9996	3
						DGAGDVAFVK	2	0.9686	1
						DLFRDDTVCLAK	2	0.9735	1
						EGTCPEAPTDECKPV	2	0.9602	3
						EGTCPEAPTDECKPVK	2	0.9993	2
						EGYGYGTGAFR	2	0.9993	2
						FDFFSGEGCAPSK	2	0.9996	4
						GLLYCDLPEPR	2	0.9883	3
						HSTIFENLANK	2	0.9328	1
						IECVSAETTEDCIAK	2	0.9996	4
						KCSTSSLEACTFR	2	0.9993	4
						KPVEEYANCHLAR	2	0.9996	3
						KPVEEYANCHLAR	3	0.9959	1
						KPVEEYANCHLAR	4	0.9582	1
						LKDEWSNVSGK	2	0.9656	1
						MYLGVEYVTAIR	2	0.9995	3
						SAGWNPIGGLLYCDLPEPR	2	0.9996	4
						SAGWNPIGGLLYCDLPEPR	3	0.9205	2
						SASDLTWDNLK	2	0.9989	3
						SVIPSDGVSACVK	2	0.9739	1
						WCALSHHER	2	0.9996	4
						WCASVEHEATK	2	0.9988	1
						YCDLPEPR	2	0.9152	1
						YYGYTGAFR	2	0.9983	2
Q5565-1	P02788-2	TRFL_HUMAN	LTF	Isoform DeltaLf of Lactotransferrin	1.0000	7.51	4	4	14
						CLAENAGDVAFAK	2	0.9995	3
						LADFALLCLDGK	2	0.9995	3
						NLLFNDNTECLAR	2	0.9994	4
						VVWCAVGEQELR	2	0.9995	4
Q5566-1	P02790	HEMO_HUMAN	HPX	Hemopexin	1.0000	17.97	10	12	22
						CSPHVL	2	0.8998	1
						DSDVAAPCGSSR	2	0.9156	2
						EVGTGPHILDSDVAAPCGSSR	3	0.9957	2
						GGYTLVSGYPK	2	0.9996	2
						LHIMAGR	2	0.9845	1
						LWWLDLK	2	0.9974	1
						LVLVGQTQVYVFLTK	2	0.9996	4
						LVLVGQTQVYVFLTK	3	0.9994	3
						RLWWLDLK	2	0.9869	1
						RLWWLDLK	3	0.9952	2
						SVDAAPCGSSR	2	0.944	1
						YYCFQGNQFLR	2	0.9995	2
Q5567-1	P04003	C4BPA_HUMAN	C4BPA	C4b-binding protein alpha chain	1.0000	44.89	39	51	125
						CEWETPEGCEQVLTK	2	0.9997	4
						CEWETPEGCEQVLTKR	2	0.9997	3
						CEWETPEGCEQVLTKR	3	0.9973	2
						CHPGYKPTTDEPTTV	2	0.9934	2
						CHPGYKPTTDEPTTVICQK	2	0.9997	2
						CHPGYKPTTDEPTTVICQK	3	0.9995	3
						EDVYVVGTVLR	2	0.9997	2
						FSAICQDGTWSPR	2	0.9998	5
						FSAICQDGTWSPR	3	0.9192	1
						FSLIGHASI	2	0.9739	2
						GDEISFSCHETS	2	0.8778	1
						GVGWSHPLPQCEIVK	2	0.9996	2
						GVGWSHPLPQCEIVK	3	0.9982	1
						GVLVGQAK	2	0.9997	1
						HSGEENFYAGFSV	2	0.9147	1
						HSGEENFYAGFSVTY	2	0.9878	3
						HSGEENFYAGFSVTYSCDPR	3	0.9996	3
						KEDVYVVGTVLR	2	0.808	1
						KEIIEYCDGYILVGQAK	3	0.9116	2
						KPDVSHGEMVSGFGPIYNYK	3	0.9996	3
						KPDVSHGEMVSGFGPIYNYKDTIVFK	3	0.9974	1
						KPDVSHGEMVSGFGPIYNYKDTIVFK	4	0.9838	3
						LMQCLPNPEDVK	2	0.9997	5
						LSCSYSHWSAPAPQCK	2	0.9997	3
						LSCSYSHWSAPAPQCK	3	0.9962	1
						LSLEIEQLELQR	2	0.9997	7
						LSLEIEQLELQR	3	0.9997	3
						LSLEIEQLELQORD	2	0.9955	3
						LSLEIEQLELQORD	3	0.9017	1
						LSLEIEQLELQORDS	2	0.9873	2
						LSLEIEQLELQORDSA	2	0.9569	2
						LSLEIEQLELQORDSAR	2	0.9583	1
						LSLEIEQLELQORDSAR	3	0.9994	2
						MALEVYK	2	0.9996	2
						MALEVYKL	2	0.8233	1
						MALEVYKLSLEIEQLELQR	2	0.9961	1
						MALEVYKLSLEIEQLELQR	3	0.9993	4
						QSSSYFFKEIIEYCDGYILVGQAK	3	0.9957	5
						RLMQCLPNPEDVK	2	0.9893	3
						SAICQDGTWSPR	2	0.9802	2
						SGFGPIYNYK	2	0.984	1
						SLEIEQLELQR	2	0.991	2
						SRPANHCVPYFGDEISFSCHETS	3	0.9986	1
						SYSHWSAPAPQCK	2	0.9922	3
						TWYPEVPK	2	0.9997	2
						TWYPEVPKCEWETPEGCEQVLTK	3	0.9995	5
						TWYPEVPKCEWETPEGCEQVLTKR	3	0.9994	6
						TWYPEVPKCEWETPEGCEQVLTKR	4	0.9744	1
						WTPYGGCEALCCPEPK	2	0.9997	4
						WTPYGGCEALCCPEPK	3	0.9988	2
						YTCQLSVIR	2	0.9997	2
Q5568-1	P04004	VTNC_HUMAN	VTN	Vitronectin	1.0000	49.79	34	38	104
						AQYWLGGPAPGHL	2	0.971	2
						CQCDELCSYQSC	2	0.9731	2
						CQCDELCSYQSCCTDYAECKPQ	3	0.9796	1
						CQCDELCSYQSCCTDYAECKPQVTR	3	0.9992	3
						CTEGFNVDKK	2	0.9997	6
						CTEGFNVDKK	3	0.9989	1
						DGVLPDPYPR	2	0.9833	1
						DSWEDIFELFWGR	3	0.9994	3
						DVWGIEGPDAAFR	2	0.9998	17
						DVWGIEGPDAAFR	3	0.9997	3
						DVWGIEGPDAAFR	2	0.9513	2
						DWHGVPGQVDAAMAGR	2	0.9997	4
						DWHGVPGQVDAAMAGR	3	0.9997	3
						ERYVFFK	2	0.9592	1
						FEDGVLPDPYPR	2	0.9997	10

						FFSGDKYYR	2	0.9131	2
						GNPEQTPVLKPEEEAPEVGASKPEG	3	0.9825	2
						GQCYELDEK	2	0.9997	4
						GSQYWRFEDGVLDPDYPYR	3	0.9969	3
						IEGHDAAFR	2	0.9117	1
						MDWLVPATCEPQSVFFSGDK	2	0.9996	2
						MDWLVPATCEPQSVFFSGDKYYR	3	0.9874	1
						QYWEYQFHQPSQEECEGS	2	0.9967	1
						QYWEYQFHQPSQEECEGSS	2	0.953	1
						QYWEYQFHQPSQEECEGSSL	2	0.9004	1
						QYWEYQFHQPSQEECEGSSLAVFEHF	3	0.9353	1
						RDVWGIEGPIDAAFR	3	0.9594	2
						RDVTDPPPYR	2	0.9997	3
						RVDTVDPYPYR	3	0.9996	3
						SIAQYWLGCAPAG	2	0.9985	1
						SIAQYWLGCAPAGH	2	0.9981	3
						SIAQYWLGCAPAGHL	3	0.9996	4
						TCEPQSVFFSGDK	2	0.9713	2
						TCEPQSVFFSGDKYYR	2	0.9664	1
						TSAGTRQPPYR	2	0.9559	2
						VDTVDPYPYR	2	0.9984	2
						VWGIEGPIDAAFR	2	0.9674	1
						WGIEGPIDAAFR	2	0.8911	2
Q5569-1	P04040	CATA_HUMAN	CAT	Catalase	1.0000	12.9	4	4	8
						ADVLTTGAGNPVGDKLNVITVGPR	3	0.9956	3
						AFYVNVINEQR	2	0.9981	2
						FNTANDNVITQR	2	0.9995	1
						GPLLQVDVFTDEMAHFDR	3	0.9994	2
Q5570-1	P04080	CYTB_HUMAN	CSTB	Cystatin-B	0.9986	24.49	2	2	2
						SQVAGTNYFIK	2	0.961	1
						VHVGDEDFVHLR	3	0.9842	1
Q5571-1	P04114	APOB_HUMAN	APOB	Apolipoprotein B-100	1.0000	27.96	96	106	196
						AAIQALR	2	0.9919	1
						AALTELSGSAQAMILGVDSK	2	0.9852	1
						AASGTTGTQYEWK	2	0.9975	2
						ADSVVDLLSYNVQSGSETTYDHK	3	0.9707	1
						AEPLAFTSHDYK	2	0.9478	1
						AHLDIAGSLGHLR	3	0.9991	1
						ALVEQGFTYPEIK	2	0.9952	1
						ATFQTPDFIVPLTDLR	2	0.9985	3
						ATGVLYDVYNNK	2	0.9992	2
						AVSMPSFSLGSDVR	2	0.997	2
						DAVEKPGFTIVAFVK	3	0.9989	2
						DFSAEYEDGKYGTLQEWEGK	3	0.9813	1
						DKDDQVLLCTLDASPGDKR	3	0.9957	3
						DKIGVELTGR	2	0.9861	1
						DKIGVELTGR	3	0.9825	1
						DLKVEDIPLAR	2	0.9361	1
						EFNLQNMGLPDFHIPENFLK	3	0.9962	3
						EFQVPTFTIPK	2	0.9932	1
						ENFAGEATLQR	2	0.9995	1
						EVYGFNPEGK	2	0.9995	2
						EYSGTIASEANTYLSNK	2	0.9997	2
						FDHTNSLNAGLSLDFSSK	3	0.9675	3
						FSPVAGIVIPSFQALTAR	2	0.9997	4
						FSPVAGIVIPSFQALTAR	3	0.9904	1
						FYVQASGAK	2	0.9922	1
						GAYQNNEIK	2	0.96	1
						GFEPTLEALFGK	2	0.9997	3
						GIISALLVPPETEEAK	2	0.9969	2
						GIISALLVPPETEEAK	3	0.9849	1
						HIYAISSAALSASYK	2	0.9021	1
						IADFELPTIIPVETIEIPSIK	2	0.9997	4
						IADFELPTIIPVETIEIPSIK	3	0.999	3
						IAELSAQAIIK	2	0.9987	1
						IDDIWNLEVK	2	0.9996	5
						IEGNLIFDPNNYLPK	2	0.9997	5
						IEIPLPGGK	2	0.9987	1
						IGDGGISTATNLK	2	0.9995	2
						IGVELTGR	2	0.999	1
						IHSQFSQVELSNDQEK	3	0.9972	2
						ILGELGFASLHDLQLLGK	3	0.9752	1
						INCKVELEVPLQCSILK	3	0.9832	3
						ITENDIQIALDDAK	2	0.9996	2
						IYSLWEHSTK	2	0.9989	2
						KGNVATEISTER	2	0.9991	1
						KSISAALEHK	2	0.9935	2
						KYTYNNEAESSGVPGTADSR	2	0.9997	2
						LAAYLMLMR	2	0.9995	1
						LAPGELTIL	2	0.9612	1
						LDNIYSSDKPYK	2	0.9978	2
						LELELRPTGEGQKVSATYELQR	3	0.9993	3
						LELELRPTGEGQKVSATYELQREDR	4	0.9872	1
						LNTDIAGLASAIDMSTNYNSDSLHFSNVFR	3	0.9994	4
						LPYTIITTPPKDFSLWEK	3	0.9412	2
						LSLSLTSYFSESSTK	2	0.9997	2
						LSLSLTSYFSESSTK	3	0.9754	1
						LSLPDFK	2	0.9983	1
						LTIFKTEL	2	0.9947	2
						LTLDIQNK	2	0.9992	1
						LTLDIQNK	2	0.9966	1
						NFVASHIANILNSEELDIQDLK	3	0.9982	2
						NFVASHIANILNSEELDIQDLK	3	0.9989	3
						NHLQLEGLFFTNGEHTSK	3	0.9798	1
						NLONNAEWYQOGAIR	2	0.9997	2
						NLONNAEWYQOGAIR	3	0.8835	1
						NMEVSATTTK	2	0.9417	1
						NNALDEVTK	2	0.9941	1
						NSEEFAAAMSR	2	0.9991	2
						NSLKEIPLPGGK	3	0.9978	2
						NTASKYENVELTK	2	0.9778	1
						QSMTLSSVQIPDFVDLGTILR	2	0.9978	1
						QSMTLSSVQIPDFVDLGTILR	3	0.9806	2
						QTIIVLENVQR	2	0.9986	2
						QTVNLQLQPSYSLVTTLSNLDK	2	0.9979	3
						QVFLYPEKDEPTYLNIK	3	0.9865	1
						QVFLYPEKDEPTYLNIK	3	0.9936	2
						SELAHWSRAK	3	0.9477	1
						SEYQADYESLR	2	0.9997	2
						SISAALEHK	2	0.9969	1
						SKPTVSSMEFK	2	0.99	2
						SPAFTDLHLR	2	0.9987	2
						SPAFTDLHLR	3	0.9996	1
						SVSDGIAALDNLAVANK	2	0.9997	5
						SVSLPSLPASAK	2	0.9585	1
						TEHGSEMLFFGNAIEGK	3	0.9977	1
						TEVIPPUEINR	2	0.9965	2
						TGISPLALIK	2	0.9995	2
						TLADLTLLDSPIK	2	0.9995	1
						TOFNNNISQDLDAYNTK	2	0.9997	2
						TSSFALNIUPTPEVKFPEVDLTK	3	0.9978	3
						TTLTAFGFASADIEIGLEGK	2	0.9997	4
						VEKPGQFTIVAFVK	3	0.9829	2

							VELEVPQLCSFIK	2	0.9992	2
							VLAQKFIIRLIK	3	0.9394	2
							VLDQQLGTTSIFR	2	0.9853	1
							VNWEEEAASGLTSLK	2	0.9995	1
							VNWEEEAASGLTSLK	3	0.9977	1
							VNWEEEAASGLTSLKDNVPK	3	0.9981	4
							VPSYTLPLSLPLVLVHVPR	3	0.9995	4
							VQGVFESH	2	0.9984	1
							VQGVFESH	3	0.9905	1
							VSALLTPAEQTGTWK	2	0.9991	2
							YDNQQDVHSINLPFFETLQEFER	3	0.9719	1
							YEDGTLSTLSTSLDQSGIHK	2	0.9997	4
							YHWEHTGLTLR	3	0.9781	1
							YNALDLTNNKG	2	0.9782	2
							YTYNYEASSSGVPTGADSR	2	0.9969	1
Q5572-1	P04196	HRG_HUMAN	HRG	Histidine-rich glycoprotein	1.0000		30.86	23	28	52
							ADLFYDYVEALDLESPK	2	0.9998	4
							ADLFYDYVEALDLESPK	3	0.9997	1
							ALDUNK	2	0.9977	1
							ALDUNKR	2	0.9993	1
							DGYLFQLLR	2	0.9997	5
							DSPVLIDFFEDTER	2	0.9998	7
							DSPVLIDFFEDTERYR	2	0.9612	1
							DVQESDCSVLSR	2	0.9711	2
							HPNVFGFCR	2	0.9963	1
							HPNVFGFCR	3	0.9983	1
							KYWNDCPEPPDSR	2	0.9997	1
							KYWNDCPEPPDSR	3	0.9578	1
							LVLVDVQESDCSVLSR	2	0.9451	1
							NLVINCEVDPQEH	2	0.9591	1
							NLVINCEVDPQEHEN	2	0.9666	2
							NLVINCEVDPQEHENI	2	0.9725	1
							RDGYLFQLLR	2	0.9612	1
							RDGYLFQLLR	3	0.9996	4
							RPSEIVGQCK	2	0.9997	2
							RPSEIVGQCK	3	0.9941	1
							RRDGYLFQLLR	3	0.9983	2
							SGFPQVSMFFTHTFPK	2	0.999	2
							SPVLIDFFEDTER	2	0.9857	2
							VRGGEGTGTVDFSVR	2	0.9962	2
							YDVEALDLESPK	2	0.9847	2
							YKEENDOFASFR	3	0.9914	1
							YKEENDOFASRVDR	2	0.9378	1
							YWNDCPEPPDSR	2	0.9985	1
Q5573-1	P04217	A1BG_HUMAN	A1BG	Alpha-1B-glycoprotein	1.0000		19.39	8	8	19
							ALGDGGHYTCR	2	0.9754	1
							ATWSGAVLAGR	2	0.9996	3
							AVALGDGGHYTCR	2	0.9321	1
							CEGPDPVTFELLR	2	0.9996	4
							GVTFLLR	2	0.9723	1
							SGLSTGWYTLQSK	2	0.9824	2
							TPGAAANLELIVFGPQHAGNYR	3	0.9996	4
							VTLTVCAPLSGVDFQLR	2	0.9991	3
Q5574-1	P04217-2	A1BG_HUMAN	A1BG	Isoform 2 of Alpha-1B-glycoprotein	1.0000		19.03	5		15
							ATWSGAVLAGR	2	0.9996	3
							CEGPDPVTFELLR	2	0.9996	4
							GVTFELLR	2	0.9723	1
							TPGAAANLELIVFGPQHAGNYR	3	0.9996	4
Q5575-1	P04259	K2C6B_HUMAN	KRT6B	Keratin, type II cytoskeletal 6B	1.0000		27.3	10	10	23
							ADTLTDEINFLR	2	0.9995	3
							ALYDAELSQMQTSHSDTSVVLMDNNR	3	0.9992	3
							DVDAAYMKNKVELQAK	2	0.9988	2
							GSGGLGGACGGAGGFSR	2	0.9984	2
							ISIGGSGAISGGYGS	2	0.9994	2
							LLKEYQELMMVK	2	0.9981	3
							NKLEGLEDALCK	3	0.9118	1
							QCANLQAIADAEQR	2	0.9873	2
							QNLEPLFEQYINNLR	2	0.9977	3
							SRAEASWYQTK	2	0.9945	2
Q5576-1	P04264	K2C1_HUMAN	KRT1	Keratin, type II cytoskeletal 1	1.0000		69.1	41	54	116
							AEAESLYQSK	2	0.9989	1
							AEAESLYQSKYEELQITAGR	3	0.9575	1
							AQYEDIAQK	2	0.9995	1
							DVDGAYMTK	2	0.999	2
							DYQELMNTK	2	0.9988	1
							ELLOQVDTSTR	2	0.9816	1
							FLEQQNQVLQTK	2	0.9997	3
							FLEQQNQVLQTKWELQQQVDTSTR	3	0.9987	3
							GGGGGGYSGSGSGSGSGSGSGSGSGSGSGSG	2	0.9987	3
							GGGGGGYSGSGSGSGSGSGSGSGSGSGSGSGGGR	3	0.9996	3
							GGGGGSGFAGGGGFSR	2	0.8341	1
							GGSGGGGGSGSGSGSGSGSGSGSGSGSGSGSGVVK	3	0.9527	1
							GSYSGSGSGSYSGSGSGSGSGSGSGSGSGSGSGSGYR	3	0.9994	2
							KQISNLQQSISDAEQR	3	0.8333	1
							LDNLQQEIDFLTALYQAELSOMQTQISETNVILSMDNNR	4	0.9928	3
							LDSELKNMQDMVEDYR	3	0.8465	1
							LEQQNQVLQTK	2	0.9924	1
							LNLDLEDALQQAK	2	0.9996	2
							LNLDLEDALQAKEDLAR	2	0.9826	1
							LNLDLEDALQAKEDLAR	3	0.8112	1
							MSGECAPNVSVSVSTSHHTISGSGSR	3	0.9996	3
							NKLNLDLEDALQQAK	2	0.9986	2
							NKLNLDLEDALQQAK	3	0.9959	1
							NKLNLDLEDALQAKEDLAR	2	0.9985	2
							NKLNLDLEDALQAKEDLAR	3	0.9991	3
							NMQDMVEDYR	2	0.9995	2
							NSKIEISELNR	2	0.9811	2
							NSKIEISELNR	3	0.9979	1
							QISNLQQSISDAEQR	2	0.9997	3
							QISNLQQSISDAEQR	3	0.9994	1
							SDQSRDLDELK	2	0.9963	1
							SGGGFSGSGAGIINYQR	2	0.9995	3
							SISISVAR	2	0.9747	1
							SKAEAEVLYQSKYEELQITAGR	3	0.9993	4
							SLDLSHAEVK	2	0.9987	3
							SLDLSHAEVK	3	0.9954	2
							SLQPINVEIDPEIQK	2	0.9945	2
							SLQPINVEIDPEIQK	3	0.8668	2
							SLNNQFASIDK	2	0.9996	1
							SLNNQFASIDKVR	2	0.9989	3
							SLNNQFASIDKVR	3	0.9881	2
							SLVNLGGSKSISISVAR	3	0.9376	2
							THNLEPYFESFINNLR	2	0.9995	6
							THNLEPYFESFINNLR	3	0.9997	5
							THNLEPYFESFINNLR	2	0.8671	1
							THNLEPYFESFINNLR	3	0.999	3
							THNLEPYFESFINNLR	4	0.9962	4
							TINQSLQPINVEIDPEIQK	2	0.9925	3
							TLEGEESR	2	0.999	2
							TNAENEFVTIK	2	0.9996	2
							TNAENEFVTIKK	2	0.9994	5
							TNAENEFVTIKK	3	0.9948	1

						WELLQQVDTR	2	0.9997	3
						YEEQLTAGR	2	0.9997	2
Q5577-1	P04350	TB84A_HUMAN	TUBB4A	Tubulin beta-4A chain	1.0000	7.66	3	3	8
						ALTVPQLTQMFDAK	2	0.9994	4
						GHYTEGAELVDAVLVVR	3	0.9989	3
						GHYTEGAELVDAVLVVR	3	0.9891	1
Q5578-1	P04406	G3P_HUMAN	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	1.0000	65.67	24	29	84
						AGAAYVVESTGVFTTMEK	2	0.8445	1
						GALQNIIPASTGAAK	2	0.9997	3
						GILGYTEHQVSSD	2	0.8054	1
						GILGYTEHQVSSD	4	0.9881	3
						GILGYTEHQVSSDFNSDTHSTFDAGAGIALNDHFVK	2	0.9997	4
						IISNASCTNCLAPLAK	3	0.8098	1
						IISNASCTNCLAPLAK	3	0.8098	1
						ISWYDNEFGYSNR	2	0.9884	2
						LEKPAKYDDIK	2	0.9917	3
						LEKPAKYDDIKK	2	0.999	4
						LISWYDNEFGYSNR	2	0.9998	9
						LISWYDNEFGYSNR	3	0.9993	3
						LTGMAFR	2	0.9971	1
						LTGMAFRVPTANVSVVOLTCTCR	3	0.9994	3
						LVINGNPITIFQER	2	0.9996	2
						LVINGNPITIFQERD	2	0.9461	1
						LVINGNPITIFQERDPSK	2	0.995	1
						SWYDNEFGYSNR	2	0.9964	3
						VDIVAINDPIDLNLY	2	0.9381	1
						VDIVAINDPIDLNLYMVMFMQYDSTHGK	3	0.9949	3
						VIHDFGIVEGLMTTV	2	0.9446	1
						VIHDFGIVEGLMTTVHAI	3	0.9769	1
						VIHDFGIVEGLMTTVHAITATQK	3	0.9996	11
						VIHDFGIVEGLMTTVHAITATQK	4	0.9981	4
						VPTANVSVVOLTCTCR	2	0.9998	5
						VSVVOLTCTCR	2	0.8801	1
						VVDLMAHMASKE	2	0.9997	2
						VVDLMAHMASKE	3	0.9841	2
						WGDAGAAYVVESTGVFTTMEK	2	0.9997	5
						WGDAGAAYVVESTGVFTTMEK	3	0.9996	3
Q5579-1	P04406-2	G3P_HUMAN	GAPDH	Isoform 2 of Glyceraldehyde-3-phosphate dehydrogenase	1.0000	65.53	20	25	78
						AGAAYVVESTGVFTTMEK	2	0.8445	1
						GALQNIIPASTGAAK	2	0.9997	3
						GILGYTEHQVSSDFNSDTHSTFDAGAGIALNDHFVK	4	0.9881	3
						IISNASCTNCLAPLAK	2	0.9997	4
						IISNASCTNCLAPLAK	3	0.8098	1
						ISWYDNEFGYSNR	2	0.9884	2
						LEKPAKYDDIK	2	0.9917	3
						LEKPAKYDDIKK	2	0.999	4
						LISWYDNEFGYSNR	2	0.9998	9
						LISWYDNEFGYSNR	3	0.9993	3
						LTGMAFR	2	0.9971	1
						LTGMAFRVPTANVSVVOLTCTCR	3	0.9994	3
						LVINGNPITIFQER	2	0.9996	2
						LVINGNPITIFQERD	2	0.9461	1
						LVINGNPITIFQERDPSK	2	0.995	1
						SWYDNEFGYSNR	2	0.9964	3
						VIHDFGIVEGLMTTV	2	0.9446	1
						VIHDFGIVEGLMTTVHAI	3	0.9769	1
						VIHDFGIVEGLMTTVHAITATQK	3	0.9996	11
						VIHDFGIVEGLMTTVHAITATQK	4	0.9981	4
						VPTANVSVVOLTCTCR	2	0.9998	5
						VVDLMAHMASKE	2	0.9997	2
						VVDLMAHMASKE	3	0.9841	2
						WGDAGAAYVVESTGVFTTMEK	2	0.9997	5
						WGDAGAAYVVESTGVFTTMEK	3	0.9996	3
Q5580-1	P04792	HSPB1_HUMAN	HSPB1	Heat shock protein beta-1	1.0000	67.32	18	25	100
						AQLGGPEAAK	2	0.9996	1
						AQLGGPEAAKSDETA	2	0.8581	1
						AQLGGPEAAKSDETA	2	0.9996	7
						DGVVEITGK	2	0.9995	2
						DGVVEITGKHEER	2	0.9995	2
						DGVVEITGKHEER	3	0.8002	1
						GPSWDFR	2	0.997	2
						GPSWDFRDRWYPHSR	2	0.9863	2
						GPSWDFRDRWYPHSR	3	0.9979	2
						GPSWDFRDRWYPHSR	4	0.9547	1
						KYTLPPGVDPQTQSSSLSPGTLTVEAPMPK	3	0.9997	12
						KYTLPPGVDPQTQSSSLSPGTLTVEAPMPK	4	0.9954	3
						KYTLPPGVDPQTQSSSLSPGTLTVEAPMPKL	3	0.9916	6
						LATQSEITIPVTFESR	2	0.9997	6
						QDEHGYSIR	2	0.9926	1
						QLSSGVSEIR	2	0.9994	1
						RVPFSLR	2	0.9929	1
						SLDVNHFAPELTVK	2	0.9512	2
						TKDGVVEITGK	2	0.9996	4
						TKDGVVEITGK	3	0.9994	3
						TKDGVVEITGKHEER	2	0.9996	19
						TKDGVVEITGKHEER	3	0.9994	7
						VSLDVNHFAPELTVK	2	0.9997	5
						VSLDVNHFAPELTVK	3	0.9996	4
						YTLPPGVDPQTQSSSLSPGTLTVEAPMPK	3	0.9994	5
Q5581-1	P04844	RPN2_HUMAN	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	1.0000	10.94	4	4	6
Q5581-2	P04844-2	RPN2_HUMAN	RPN2	Isoform 2 of Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	1.0000	11.22	4	4	6
						FSSGYDFLVEVEGDNR	2	0.979	1
						NFESLSEAFSVASAAVLSHNR	3	0.9972	1
						SIVEIEDLVAR	2	0.9997	3
						TSFTIPVGDVFELNFMNVK	2	0.9498	1
Q5582-1	P04899	GNAI2_HUMAN	GNAI2	Guanine nucleotide-binding protein G(i) subunit alpha-2	1.0000	14.65	4	5	7
						EYTHFTCATDTK	2	0.9958	2
						IHEDGYSEECR	2	0.9977	1
						LLLLGAGESGK	2	0.958	1
						NVQVFDAVTDVIK	2	0.9937	1
						NVQVFDAVTDVIK	3	0.9912	2
Q5583-1	P04899-2	GNAI2_HUMAN	GNAI2	Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-2	1.0000	12.09	3	4	6
Q5583-2	P04899-3	GNAI2_HUMAN	GNAI2	Isoform 3 of Guanine nucleotide-binding protein G(i) subunit alpha-2	1.0000	12.89	3	4	6
Q5583-3	P04899-5	GNAI2_HUMAN	GNAI2	Isoform 5 of Guanine nucleotide-binding protein G(i) subunit alpha-2	1.0000	12.09	3	4	6
Q5583-4	P04899-6	GNAI2_HUMAN	GNAI2	Isoform 6 of Guanine nucleotide-binding protein G(i) subunit alpha-2	1.0000	13.53	3	4	6
						EYTHFTCATDTK	2	0.9958	2
						IHEDGYSEECR	2	0.9977	1
						NVQVFDAVTDVIK	2	0.9937	1
						NVQVFDAVTDVIK	3	0.9912	2
Q5584-1	P04899-4	GNAI2_HUMAN	GNAI2	Isoform sG(i) of Guanine nucleotide-binding protein G(i) subunit alpha-2	1.0000	10.11	3	3	4
						EYTHFTCATDTK	2	0.9958	2
						IHEDGYSEECR	2	0.9977	1
						LLLLGAGESGK	2	0.958	1
Q5585-1	Q9BTM1	H2AJ_HUMAN	H2AFJ	Histone H2A.J	1.0000	21.71	4	5	8
Q5585-2	Q9BTM1-2	H2AJ_HUMAN	H2AFJ	Isoform 2 of Histone H2A.J	1.0000	18.54	4	5	8
Q5585-3	P16104	H2AX_HUMAN	H2AFX	Histone H2AX	1.0000	19.58	4	5	8
Q5585-4	P04908	H2A1B_HUMAN	HIST1H2AB	Histone H2A type 1-B/E	1.0000	21.54	4	5	8
Q5585-5	Q93077	H2A1C_HUMAN	HIST1H2AC	Histone H2A type 1-C	1.0000	21.54	4	5	8
Q5585-6	P20671	H2A1D_HUMAN	HIST1H2AD	Histone H2A type 1-D	1.0000	21.54	4	5	8
Q5585-7	P0C058	H2A1E_HUMAN	HIST1H2AE	Histone H2A type 1-E	1.0000	21.54	4	5	8
Q5585-8	Q96KKS	H2A1H_HUMAN	HIST1H2AH	Histone H2A type 1-H	1.0000	21.54	4	5	8
Q5585-9	Q99878	H2A1J_HUMAN	HIST1H2AJ	Histone H2A type 1-J	1.0000	21.88	4	5	8
Q5585-10	Q8UIE6	H2A2B_HUMAN	HIST2H2AB	Histone H2A type 2-B	1.0000	21.54	4	5	8
Q5585-11	Q7L7L0	H2A3_HUMAN	HIST3H2A	Histone H2A type 3	1.0000	21.54	4	5	8

						AGLQFPVGR	2	0.9832	1
						AVLEYLTAEILELAGNAAR	2	0.9332	1
						AVLEYLTAEILELAGNAAR	3	0.9888	3
						EILELAGNAAR	2	0.8606	1
						VLEYLTAEILELAGNAAR	3	0.9791	2
Q5586-1	P05023-3	AT1A1_HUMAN	ATP1A1	Isoform 3 of Sodium/potassium-transporting ATPase subunit	1.0000	5.14	4	4	5
Q5586-2	P05023-4	AT1A1_HUMAN	ATP1A1	Isoform 4 of Sodium/potassium-transporting ATPase subunit	1.0000	4.99	4	4	5
Q5586-3	P05023	AT1A1_HUMAN	ATP1A1	Sodium/potassium-transporting ATPase subunit alpha-1	1.0000	4.99	4	4	5
						GIVVYTGDR	2	0.9906	1
						GVGISEGNETVEDIAAR	2	0.9996	2
						LIIVEGQCR	2	0.9945	1
						NIAFFSTNCVEGTAR	2	0.9991	1
Q5587-1	P05060	SCG1_HUMAN	CHGB	Secretogranin-1	0.9635	1.77	1	1	2
						CIEVLSNALS	2	0.9635	2
Q5588-1	P05062	ALDOB_HUMAN	ALDOB	Fructose-bisphosphate aldolase B	1.0000	10.99	3	3	6
						IADQCPSSLAIQENANALAR	2	0.9996	3
						LDQGGAPLAGTNK	2	0.9992	2
						LSFSYGR	2	0.9834	1
Q5589-1	P05067	A4_HUMAN	APP	Amyloid beta A4 protein	1.0000	20.39	12	13	24
Q5589-2	P05067-11	A4_HUMAN	APP	Isoform 11 of Amyloid beta A4 protein	1.0000	21.05	12	13	24
Q5589-3	P05067-8	A4_HUMAN	APP	Isoform APP751 of Amyloid beta A4 protein	1.0000	20.91	12	13	24
Q5589-4	P05067-7	A4_HUMAN	APP	Isoform L-APP733 of Amyloid beta A4 protein	1.0000	21.42	12	13	24
Q5589-5	P05067-9	A4_HUMAN	APP	Isoform L-APP752 of Amyloid beta A4 protein	1.0000	20.88	12	13	24
						CAPFFYGGCGGNR	2	0.9997	2
						CLVGEFVSALLVPDKCK	2	0.9974	1
						CLVGEFVSALLVPDKCK	3	0.9913	1
						EVCSQAETGPCR	2	0.9997	3
						ISYGNDALMPSLTETK	2	0.9989	2
						LALENYITALQAVPPRRP	3	0.9754	1
						LNMMHMNVQNGK	2	0.8631	1
						QQLVETHMAR	2	0.9832	1
						SQVMTHLR	2	0.9979	2
						STNLHDYGMLLPGDGKFR	3	0.9475	1
						THPHFVIPYR	3	0.9994	3
						VESLEGEAANER	2	0.9975	2
						WYFDVTEGK	2	0.9997	4
Q5590-1	P05090	APOD_HUMAN	APOD	Apolipoprotein D	1.0000	47.09	18	23	59
						CPNPPVQENFDVVK	2	0.9997	5
						CPNPPVQENFDVVK	3	0.9993	2
						CPNPPVQENFDVKNYLGR	2	0.9995	5
						CPNPPVQENFDVKNYLGR	3	0.9994	3
						DSKNILTSNNIDVK	2	0.9402	1
						HVDFAWILAR	2	0.8847	1
						IKVLNGELR	2	0.9804	1
						IKVLNGELR	3	0.8852	1
						IPPTFENGR	2	0.9724	1
						KMTVTDQVNCCK	2	0.9997	2
						KMTVTDQVNCCK	3	0.9994	1
						MTVTDQVNCCK	2	0.9996	2
						MTVTDQVNCCK	2	0.9718	1
						NILTSNNIDVK	2	0.9997	4
						NILTSNNIDVKK	2	0.9997	1
						NPNLPETVDSLK	2	0.9997	11
						NPNLPETVDSLK	3	0.986	2
						NPNLPETVDSLK	2	0.9905	2
						VLNQELR	2	0.9994	2
						WYIEKIPTTF	2	0.9158	2
						WYIEKIPTTF	2	0.963	2
						WYIEKIPTTFENGR	2	0.9992	6
						WYIEKIPTTFENGR	3	0.9986	1
Q5591-1	P05109	S10A8_HUMAN	S10A8	Protein S100-A8	1.0000	75.27	19	23	65
						ALNSIDVVH	2	0.9799	1
						ALNSIDVVHK	2	0.9996	3
						ALNSIDVVHK	3	0.9993	3
						ALNSIDVVHKY	2	0.9946	3
						ALNSIDVVHKY	3	0.9515	1
						ALNSIDVVHKYSLIK	2	0.9927	2
						ELDINTDGAVNFQK	2	0.8167	1
						ELDINTDGAVNFQK	3	0.9996	18
						GADVWFK	2	0.9996	2
						GADVWFK	3	0.9952	2
						GADVWFK	2	0.9996	3
						GNFHAVYR	2	0.9996	3
						GNFHAVYRDDLK	2	0.9989	3
						GNFHAVYRDDLK	3	0.9709	1
						GNFHAVYRDDLK	2	0.9956	4
						KGADVWFK	2	0.9955	1
						KGADVWFK	2	0.9816	2
						KLLETCQYIR	2	0.9996	4
						KLLETCQYIR	3	0.9973	2
						LETETCPQYIR	2	0.9893	1
						LETETCPQYIR	2	0.9996	3
						LETETCPQYIR	2	0.9993	2
						NFQEFLLVIK	2	0.9842	2
						QEFULLVIK	2	0.9756	1
Q5592-1	P05154	IPSP_HUMAN	SERPINA5	Plasma serine protease inhibitor	1.0000	28.57	11	12	24
						AAAATGTFTR	2	0.9997	3
						AVVEVDESCTR	2	0.9997	2
						DFTDLVR	2	0.9995	2
						EDQYHYLLDR	2	0.8973	1
						FSIEGYSQLEK	2	0.9965	2
						GFOQLLQELNQPR	2	0.9993	3
						GFOQLLQELNQPR	3	0.9996	2
						GTQEQDFYVYSETVVR	2	0.9997	3
						MOILEGLGLNLQK	2	0.9994	2
						QLELPLK	2	0.9636	1
						RDTFDLYR	2	0.9422	1
						TLYLDATFTNFR	2	0.9997	2
Q5593-1	P05164-2	PERM_HUMAN	MPO	Isoform H14 of Myeloperoxidase	1.0000	19.23	10	10	23
Q5593-2	P05164-3	PERM_HUMAN	MPO	Isoform H7 of Myeloperoxidase	1.0000	16.09	10	10	23
Q5593-3	P05164	PERM_HUMAN	MPO	Myeloperoxidase	1.0000	16.78	10	10	23
						AVSNEIVRFPDQLTPDQER	3	0.9811	2
						FPTDQLTPDQER	2	0.9992	6
						IANVTNAFR	2	0.9982	1
						IICDNTGITTVSK	2	0.9822	2
						IICDNTGITTVSKN	2	0.9772	2
						IPCLAGDTR	2	0.9975	2
						SLMFMDWGQLLDHIDFTPEAAR	3	0.9829	1
						VGPIILACIGTQFR	2	0.9993	3
						VVLEGGIDPLR	2	0.9985	3
						WLPAYEYDGLSLPYGWTPGVK	2	0.9963	1
Q5594-1	P05386	RLA1_HUMAN	RPLP1	60S acidic ribosomal protein P1	1.0000	14.04	1	2	5
						AAGNVVEFPWPGLFAK	2	0.9997	3
						AAGNVVEFPWPGLFAK	3	0.9956	2
Q5595-1	P05387	RLA2_HUMAN	RPLP2	60S acidic ribosomal protein P2	1.0000	48.7	5	5	8
						ILDSVGIEADDDRLNK	2	0.9992	3
						KILDSVGIEADDDRLNK	3	0.9795	1
						NIEDVIAQGIGK	2	0.9993	2
						VISELGNKNEVDIAQGIGK	3	0.9102	1
						YVASTLLAALGNSPSAK	2	0.999	1
Q5596-1	P05388	RLA0_HUMAN	RPLP0	60S acidic ribosomal protein P0	1.0000	35.65	9	10	18
						AGAIAPCEVTVPAQNTGLGPEK	2	0.9996	2
						AGAIAPCEVTVPAQNTGLGPEK	3	0.8427	1
						CFIVGADNVGSK	2	0.992	1

						GHLENNPALEK	2	0.9986	3
						GNVGFVFTK	2	0.9943	1
						GNVGFVTEKDELTEIR	3	0.9979	1
						GTEILSDVQLIK	2	0.9994	1
						IIQLDDYPK	2	0.9994	2
						TSFFQALGITTK	2	0.9997	3
Q5597-1	P05534	1A24_HUMAN	HLA-A	HLA class I histocompatibility antigen, A-24 alpha chain	1.0000	VLALSVETDITFLPAEK	2	0.9997	3
						20.82	5	5	10
						APWIEQEGPEYDEETGKVK	3	0.9961	3
						ATLEGTCVDGLR	2	0.9973	1
						CWALGFYPAEITLTWQR	2	0.9996	2
						FIAGVVDOTQFVR	2	0.9996	2
Q5598-1	P05543	THBG_HUMAN	SERPINA7	Thyroxine-binding globulin	1.0000	WAAVVVPSGEEQR	2	0.9989	2
						4.58	2	2	4
						NALALFVLPK	2	0.9991	2
						SFMLILR	2	0.9996	2
Q5599-1	P05546	HEP2_HUMAN	SERPIND1	Heparin cofactor 2	1.0000	38.48	26	30	69
						DALENIDPATQMMILNCIFYK	2	0.9907	1
						EYFAAQADJDS	2	0.9738	2
						EYFAAQADJDSAPAFISK	2	0.9997	5
						FAFNLYR	2	0.9994	2
						FTVDRPFLF	2	0.9958	8
						FTVDRPFLFUYEHR	2	0.9992	3
						FTVDRPFLFUYEHR	3	0.9996	6
						FTVDRPFLFUYEHR	4	0.9994	4
						GPLDQLEK	2	0.9837	1
						HQGTITVNEEGTQ	2	0.9953	2
						HQGTITVNEEGTQA	2	0.9635	2
						HQGTITVNEEGTQAT	2	0.9865	2
						HQGTITVNEEGTQATT	2	0.9899	3
						HQGTITVNEEGTQATTV	2	0.9937	2
						HQGTITVNEEGTQATTVT	2	0.994	2
						IAIDLFK	2	0.9966	1
						LNVPHK	2	0.8948	1
						LNILNAK	2	0.99	1
						MLFDKNGNMAGISDQR	2	0.9966	3
						MLFDKNGNMAGISDQR	3	0.9988	2
						NFGYTLR	2	0.9974	1
						NGNMAGISDQR	2	0.9985	1
						NYNLVESLK	2	0.9991	2
						QFPILLDFK	2	0.9989	2
						RNFGYTLR	2	0.9964	1
						SVNDLYIQK	2	0.9898	1
						TLEAQITPR	2	0.9988	2
						TSCLLFMR	2	0.9996	2
						YEITTHNLFR	2	0.9996	2
						YEITTHNLFR	3	0.9979	2
Q5600-1	P05787-2	K2C8_HUMAN	KRT8	Isoform 2 of Keratin, type II cytoskeletal 8	1.0000	41.68	23	27	54
Q5600-2	P05787	K2C8_HUMAN	KRT8	Keratin, type II cytoskeletal 8	1.0000	44.1	23	27	54
						AQYEDIANR	2	0.9966	2
						ASLEAAIAAEQR	2	0.9992	2
						ASLEAAIAAEQR	3	0.9992	2
						ASLEAAIAAEQRGELAIAK	3	0.9643	1
						ASLEAAIAAEQRGELAIAKANAK	3	0.9894	2
						DVDEAYMKNKVELES	2	0.9996	2
						DVDEAYMKNKVELES	3	0.999	1
						DVDEAYMKNKVELESGLDGEINFLR	3	0.8179	1
						ELQSQSDTSVLSMDNSR	2	0.9997	2
						EYQELMNVK	2	0.9948	1
						KLLEGEESR	2	0.9986	2
						LALDIEATYRK	2	0.9972	1
						LEAELGNMQGLVEDFK	2	0.9997	3
						LEGLTDEINFLR	2	0.9997	5
						LEGLTDEINFLR	3	0.9926	2
						LKLEAELGNMQGLVEDFK	2	0.9995	3
						LKLEAELGNMQGLVEDFK	3	0.999	3
						LSEEAALQR	2	0.9996	2
						QLETGGQEK	2	0.9979	1
						QLYEEERELQSQSDTSVLSMDNSR	3	0.9963	3
						RLQLETGGQEK	2	0.9916	1
						SLDMSIAEYK	2	0.9997	3
						SNMDNMFESYNNLR	2	0.9997	2
						TEMENEFVLJK	2	0.9958	3
						TEMENEFVLKK	2	0.9995	1
						TKTEISEMNR	2	0.9862	2
						YEELQSLAGK	2	0.9954	1
Q5601-1	P06310	KV206_HUMAN		Ig kappa chain V-II region RPMI 6410	1.0000	9.77	1	1	2
						FSGSGSGTDFTLK	2	0.9993	2
Q5602-1	P06396	GELS_HUMAN	GSN	Gelsolin	1.0000	25.96	16	16	34
Q5602-2	P06396-2	GELS_HUMAN	GSN	Isoform 2 of Gelsolin	1.0000	27.77	16	16	34
Q5602-3	P06396-3	GELS_HUMAN	GSN	Isoform 3 of Gelsolin	1.0000	27.36	16	16	34
Q5602-4	P06396-4	GELS_HUMAN	GSN	Isoform 4 of Gelsolin	1.0000	27.47	16	16	34
						AGALNSNDAPVLK	2	0.9995	3
						AGKEPGLQIWR	3	0.9852	1
						AQPQVQVAEGSPDGFWEALGGK	2	0.9996	1
						DFFTGDAYVLK	2	0.9495	2
						DSQEEKTEALTSK	2	0.9916	2
						EVQGFESATFLGYK	2	0.9997	6
						HVPNEVVVQR	2	0.9982	1
						IEGSKNVFDPATYQGYGGDSYILYNR	3	0.9995	4
						NLYGDFFTGDAYVLK	2	0.8426	1
						QTQVSVLPGETPLFK	2	0.997	2
						TGAQELLR	2	0.99	1
						TPITVVK	2	0.9952	1
						TPSAAYLWVYGTGASEAEK	2	0.9997	2
						TPSAAYLWVYGTGASEAEKGAQELLR	3	0.9975	2
						VEKFDLVPVPTNLYGDFFTGDAYVLK	3	0.9951	3
						YIETDPANR	2	0.9943	2
Q5603-1	P06576	ATP8_HUMAN	ATP5B	ATP synthase subunit beta, mitochondrial	1.0000	32.51	12	15	29
						AHGGYSVFAGVGR	2	0.9988	2
						AHGGYSVFAGVGR	3	0.9452	1
						AIAELGYPVDPDLDSR	2	0.9987	2
						DQEGQDVLLFDINFR	2	0.9997	2
						FTQAGSEVALLGR	2	0.9997	3
						LVLEVAQHIGESTVR	2	0.9997	3
						LVLEVAQHIGESTVR	3	0.9431	1
						SLQDIHAKQNDLSEKDLTVSR	3	0.8566	1
						TVLIMELINNAK	2	0.9997	2
						VALTGLTVAEYFR	2	0.9991	3
						VALTGLTVAEYFRDQEGQDVLLFDINFR	3	0.9994	3
						VALTGLTVAEYFRDQEGQDVLLFDINFR	4	0.813	1
						VALVYQMNEPPGAR	2	0.965	1
						VLDSGAPIKIPVGPETLGR	3	0.9981	3
						VVDLLAPYAK	2	0.9968	1
Q5604-1	P06681	CO2_HUMAN	C2	Complement C2	1.0000	7.05	4	4	10
						CSSNLVLTGSSER	2	0.9988	3
						EVVTDQFLCSGTQDESCKGSGGAVFLR	3	0.9981	3
						GESGGAFLER	2	0.8935	1
						HAFILQDTK	2	0.9986	3
Q5605-1	P06702	S10A9_HUMAN	S100A9	Protein S100-A9	1.0000	67.54	21	26	66
						DIQNFLK	2	0.9995	1
						DIQNFLK	2	0.9976	2
						IETINTFHQYSVK	2	0.8736	1

						INTFHQYSVK	2	0.9945	2
						KDQNFVK	2	0.9976	2
						KDQNFVK	2	0.9883	2
						KLGHPTLNQGEFK	2	0.9951	3
						KLGHPTLNQGEFK	3	0.9691	1
						LGHPTLNQGEFK	2	0.9997	6
						LGHPTLNQGEFK	3	0.9996	4
						LGHPTLNQGEFK	2	0.9948	2
						LGHPTLNQGEFKELVRK	3	0.9052	1
						LTWASHEK	2	0.9993	3
						NIETINTF	2	0.9666	1
						NIETINTFH	2	0.878	1
						NIETINTFHQ	2	0.8537	1
						NIETINTFHQY	2	0.9974	6
						NIETINTFHQY	3	0.9805	1
						NIETINTFHQYS	2	0.9015	1
						NIETINTFHQYSV	2	0.9962	3
						NIETINTFHQYSVK	2	0.9997	10
						NIETINTFHQYSVK	3	0.9995	3
						QLSFEFIMLMAR	3	0.9992	2
						VEHIMEDLDTNADK	3	0.9995	3
						VEHIMEDLDTNADKQLSFEFIMLMAR	3	0.9987	3
						VEHIMEDLDTNADKQLSFEFIMLMAR	4	0.9439	1
Q5606-1	P06703	S10A6_HUMAN	S100A6	Protein S100-A6	0.9991	31.11	2	2	2
						DOEVNFOEYVTFGLGALALYNEALKG	3	0.9528	1
						NKDQEVNFOEYVTFGLGALALYNEALKG	3	0.9198	1
Q5607-1	P06727	APOA4_HUMAN	APOA4	Apolipoprotein A-IV	1.0000	54.55	22	28	44
						AKIDQNVVELKGR	2	0.9919	2
						AKIDQNVVELKGR	3	0.8572	1
						ALVQQMEQLR	2	0.9996	1
						DKVNSFTSTFK	2	0.9745	1
						ENADSLQASLRPHADELK	3	0.9163	1
						IDQNVVELK	2	0.986	2
						IDQNVVELKGR	2	0.9939	2
						IDQNVVELKGR	3	0.9184	1
						ISASAEELR	2	0.9997	1
						ISASAEELRQ	2	0.8468	1
						KLVPFATELHER	2	0.9945	1
						KLVPFATELHER	3	0.998	2
						LAPLAEDVR	2	0.9206	1
						LGHAGDVEGHLSELEK	4	0.9884	1
						LKEEIGKELEELR	2	0.9924	2
						LKEEIGKELEELR	3	0.9951	2
						LLPHANEVSQK	2	0.999	1
						LNINQLEGLTFQMK	2	0.998	2
						LNINQLEGLTFQMK	3	0.9915	2
						LVPFATELHER	2	0.8977	1
						RVEPYGENFNK	2	0.9964	1
						SELTQQLNALFQDK	2	0.9997	2
						SELTQQLNALFQDK	3	0.8906	1
						SELTQQLNALFQDKLGEVNTYAGDLQK	3	0.9959	3
						SLAELGGHLDQQVEEFR	2	0.9997	2
						SLAPYAGDTQEK	2	0.9982	4
						TQVNTQAEQLR	2	0.9991	2
						TQVNTQAEQLRR	2	0.9405	1
Q5608-1	P06733	ENO4_HUMAN	ENO1	Alpha-enolase	1.0000	55.3	19	21	52
						AAVPSGASTGIWEALER	2	0.9997	4
						AAVPSGASTGIWEALER	3	0.9476	1
						AGYTDKRVIGMDVAASEFFR	3	0.9957	2
						DATNVGDEGGFAPNILENK	2	0.9997	3
						EFDSDRGNPTVEVDLFTSK	3	0.8496	1
						FGANAILGSLAVCK	2	0.9996	2
						FTASAGIQVGGDLTVTNPK	2	0.9997	3
						FTASAGIQVGGDLTVTNPK	3	0.9961	2
						FTASAGIQVGGDLTVTNPKR	3	0.9955	1
						GNPTVEVDLFTSK	2	0.9997	3
						IGAEVYHNLK	2	0.9996	2
						LAMQEFMILPVGAANFR	3	0.9678	1
						SCNGLLKL	2	0.9861	1
						SFKIDYVPSVDFPDQDDWGAWQK	3	0.9992	6
						SGETEDTFADLVGLCTGQIK	3	0.9996	5
						SGKYDLDFK	2	0.995	1
						SGKYDLDFKSPDPDSR	3	0.9918	2
						VNQIGSVTESLQACK	2	0.9985	3
						VVIGMDVAASEFFR	2	0.9997	4
						YGDATNVGDEGGFAPNILENK	3	0.9877	1
						YISPDQLADLYK	2	0.9996	4
Q5609-1	P06748-2	NPM_HUMAN	NPM1	Isoform 2 of Nucleophosmin	1.0000	38.49	7	10	23
Q5609-2	P06748	NPM_HUMAN	NPM1	Nucleophosmin	1.0000	34.69	7	10	23
						GGSLPKVEAK	2	0.9322	1
						GPSVSEDIK	2	0.999	1
						MSVQPTVSLGGFEITPPVVL	2	0.9997	4
						MSVQPTVSLGGFEITPPVVL	3	0.9973	3
						MTDQEAIQDLWQWR	2	0.9994	3
						MTDQEAIQDLWQWR	3	0.9962	2
						TVSLGAGAKDELHIVEAAMNYESPIK	3	0.9995	3
						TVSLGAGAKDELHIVEAAMNYESPIK	4	0.9784	3
						VNDENEHQLSLR	2	0.9997	2
						VTLATLK	2	0.9621	1
Q5610-1	P06753-2	TPM3_HUMAN	TPM3	Isoform 2 of Tropomyosin alpha-3 chain	0.9999	10.08	2	2	3
Q5610-2	P06753-5	TPM3_HUMAN	TPM3	Isoform 5 of Tropomyosin alpha-3 chain	0.9999	10.08	2	2	3
Q5610-3	Q5VU61	Q5VU61_HUMAN	TPM3	Tropomyosin alpha-3 chain	0.9999	11.21	2	2	3
Q5610-4	Q5VU59	Q5VU59_HUMAN	TPM3	Uncharacterized protein	0.9999	10.78	2	2	3
						KIQVLQGDADDAER	3	0.9977	1
						TIDILEDKLK	2	0.9476	2
Q5611-1	P33778	H2B1B_HUMAN	HIST1H2BB	Histone H2B type 1-B	1.0000	19.05	5	5	9
Q5611-2	P06899	H2B1J_HUMAN	HIST1H2BJ	Histone H2B type 1-J	1.0000	19.05	5	5	9
Q5611-3	P23527	H2B1O_HUMAN	HIST1H2BO	Histone H2B type 1-O	1.0000	19.05	5	5	9
Q5611-4	Q16778	H2B2E_HUMAN	HIST2H2BE	Histone H2B type 2-E	1.0000	19.05	5	5	9
Q5611-5	Q8N257	H2B3B_HUMAN	HIST3H2BB	Histone H2B type 3-B	1.0000	19.05	5	5	9
						AMGIMNSFVNDIFER	2	0.9995	4
						LLPGELAK	2	0.9986	2
						MNSFVNDIFER	2	0.8689	1
						NSFVNDIFER	2	0.814	1
						SFVNDIFER	2	0.9578	1
Q5612-1	P07195	LDHB_HUMAN	LDHB	L-lactate dehydrogenase B chain	1.0000	21.26	5	5	7
						ITVVGVGQVGRACASILGK	3	0.9215	1
						IVVVTAGVR	2	0.9019	1
						LIAPVAEEATVPNNK	2	0.9996	2
						MVVESAYEVIK	2	0.9964	2
						SLADELALVDLEDK	2	0.9993	1
Q5613-1	P07203	GPX1_HUMAN	GPX1	Glutathione peroxidase 1	1.0000	34.98	5	5	5
						FQTIDIEPDIEALLSQGPSKA	2	0.9796	1
						LAAAAAQAQSVYAFSARPLAGGEPVSLGSLR	3	0.9381	1
						LITWSPVCR	2	0.9882	1
						NDVAWNFEK	2	0.9964	1
						RFQTIDIEPDIEALLSQGPSKA	2	0.9993	1
Q5614-1	P07225	PROS_HUMAN	PROS1	Vitamin K-dependent protein S	1.0000	31.66	24	31	58
						AHSCPSVWVK	2	0.9907	1
						AHSCPSVWKK	2	0.9996	3
						AHSCPSVWKK	3	0.9991	1
						ASFTCTCKPGWQGEK	2	0.9996	1
						DCKDVDECSLSPGICGTAVCK	3	0.9495	1

						DVDECSLKPSICGTAVCK	2	0.9997	2
						DVDECSLKPSICGTAVCK	3	0.9937	1
						FSAEFDNR	2	0.9947	1
						HCLTVVEK	2	0.9996	1
						IQALSLCSDDQSH	2	0.975	2
						IQALSLCSDDQSHL	2	0.9691	1
						IQALSLCSDDQSHLEF	2	0.986	2
						IQALSLCSDDQSHLEFF	2	0.9997	3
						IQALSLCSDDQSHLEFR	3	0.999	2
						ITTGGDVINGLWNMVSVLEHSISIK	3	0.9861	1
						KVESLUKPINPR	2	0.9997	2
						KVESLUKPINPR	3	0.9985	2
						NGFVMSLNKK	2	0.9966	2
						NNLELSTPLK	2	0.9975	2
						NNLELSTPLKIETISHEDLQR	2	0.9963	1
						NNLELSTPLKIETISHEDLQR	3	0.9994	3
						QSTNAVDPDLR	2	0.968	1
						SCEVSVSLPLNLDTK	2	0.9896	2
						SFQITGLTTAAR	2	0.9981	1
						SLCSDDQSHLEFR	2	0.9987	2
						SQDILLSVENTVIYR	2	0.9997	7
						SQDILLSVENTVIYR	3	0.9996	2
						SQDILLSVENTVIYRI	2	0.8994	1
						VNRRNNLELSTPLKIETISHEDLQR	3	0.9976	3
						VNRRNNLELSTPLKIETISHEDLQR	4	0.9874	2
						VYFAGFPR	2	0.9985	2
Q5615-1	P07237	PDIA1_HUMAN	P4HB	Protein disulfide-isomerase	1.0000	31.3	14	16	22
						DAPEEDHVLVLR	2	0.9576	2
						EADDIVNWLK	2	0.9972	1
						ENLLDFIK	2	0.979	1
						ILEFFGLK	2	0.9977	1
						ITFECHR	2	0.9989	1
						LAKVDATEESDLAQYGVYR	3	0.8804	1
						MDSTANEVAVK	2	0.9976	1
						NFEDVAFDEKK	2	0.9838	1
						TGPAATTLPGAAAEVSVSEVAVIGFFK	3	0.9405	1
						TGPAATTLPGAAAEVSVSEVAVIGFFKDVESDSAK	3	0.9198	1
						THILLFLPK	2	0.9987	2
						THILLFLPK	3	0.9996	2
						VDATEESDLAQYGVYR	2	0.9997	2
						YKPESELTAEAR	2	0.9994	1
						YKPESELTAEAR	3	0.9985	2
Q5616-1	P07339	CATD_HUMAN	CTSD	Cathepsin D	1.0000	YQLDKDGVVLFK	3	0.9983	2
						40.05	12	15	31
						AIGAVPLQGVNMIPEEK	2	0.9996	3
						AYWQVHLQDVEVASGLTLCK	3	0.9734	2
						EGCEAIVDTGSLMVGPDVEVR	2	0.9997	3
						FDGILGMAYPR	2	0.9997	2
						GRIPEVLK	2	0.9479	1
						ISVNNVLPFDNLMQKQ	2	0.9993	3
						ISVNNVLPFDNLMQKQ	3	0.9994	2
						KAYWQVHLQDVEVASGLTLCK	3	0.9944	1
						LLDIACWIHHK	2	0.9978	2
						LVDQNFISFYLSR	2	0.9997	3
						LVDQNFISFYLSR	3	0.999	1
						LVDQNFISFYLSRDPADQPGGELMLGGTDSK	3	0.9994	4
						QVFGAATKQPGITFAAK	2	0.9605	2
						QVFGAATKQPGITFAAK	3	0.8206	1
						VGFAEAAAR	2	0.9997	1
Q5617-1	P07384	CAN1_HUMAN	CAPN1	Calpain-1 catalytic subunit	1.0000	3.78	3	3	3
						CLQSGTLFR	2	0.9553	1
						SEQFINLR	2	0.9942	1
						YLGQDYEQLR	2	0.9992	1
Q5618-1	P07437	TB85_HUMAN	TUBB	Tubulin beta chain	1.0000	41.89	15	20	43
						ALTVPILTQVFDK	2	0.9995	6
						ALTVPILTQVFDK	3	0.996	2
						EIVHIQAGCCGNQIGAK	2	0.9987	2
						EIVHIQAGCCGNQIGAK	2	0.9967	1
						EIVHIQAGCCGNQIGAK	3	0.8544	1
						FWEVSDHEGIDPTGTGTHGSDSLQLDR	2	0.9626	1
						FWEVSDHEGIDPTGTGTHGSDSLQLDR	3	0.9997	7
						FWEVSDHEGIDPTGTGTHGSDSLQLDR	4	0.9977	2
						GHYTEGAELVDSVLDVVR	2	0.9967	1
						GHYTEGAELVDSVLDVVRK	3	0.9794	2
						ISVYNEATGGK	2	0.9997	4
						ISVYNEATGGKYVPR	2	0.9996	2
						ISVYNEATGGKYVPR	3	0.9911	1
						LHFFMPGFAPLTSR	2	0.9886	1
						LHFFMPGFAPLTSR	3	0.9695	2
						LTPPTYGDLNLHVSATMSGVTTCLR	3	0.9852	1
						MAVTFIGNSTAIQELKRR	3	0.8833	1
						NSSYFWEVNPVVK	2	0.8393	1
						TAVCDIPPR	2	0.9915	1
						YLTVAEVR	2	0.9997	4
Q5619-1	P07711	CATL1_HUMAN	CTSL	Cathepsin L1	1.0000	15.32	3	4	5
						AVATVGPISVAIDAGHESFLYK	2	0.9976	1
						AVATVGPISVAIDAGHESFLYK	3	0.9845	1
						NHCGIASASYPYTV	2	0.9993	2
Q5620-1	P07737	PROF1_HUMAN	PFN1	Profilin-1	1.0000	NSWGEWGMGGYVK	2	0.9991	1
						53.57	8	8	19
						CYEMASHLR	2	0.9873	1
						DSLLODGEFSMDLR	2	0.9995	5
						DSPSVAAVPGK	2	0.9876	2
						SLLODGEFSMDLR	2	0.9904	3
						STGGAPTFNVTVTK	2	0.9989	1
						TVYNITPAEVLGVGK	2	0.9996	5
						TKSTGGAPTFNVTVTK	2	0.9936	1
						TLVLLMGK	2	0.9462	1
Q5621-1	P07814	SYEP_HUMAN	EPRS	Bifunctional glutamate/proline--tRNA ligase	1.0000	5.75	6	6	10
						DDBLEPAPSMGAK	2	0.9829	1
						FAGGDYTTTIEFISASGR	2	0.9175	1
						GFFICDQPYEPVSPYSCK	2	0.9996	3
						INEAVECLSLK	2	0.9984	1
						KGDIQLQR	2	0.9975	2
						LQAILEDIQLTLFR	2	0.9997	2
Q5622-1	P07858	CATB_HUMAN	CTSB	Cathepsin B	1.0000	50.15	13	18	40
						DOGSCSCGWAFAVEAISDR	2	0.9998	4
						DOGSCSCGWAFAVEAISDR	3	0.9997	2
						EIRDQSCSCGWAFAVEAISDR	3	0.9825	1
						EQWPQCPTIK	2	0.9997	3
						EQWPQCPTIK	3	0.995	1
						GLVSGGLYSHVGCRRPY	2	0.9969	2
						GQDHCGIESEVAGIPR	2	0.9998	2
						GQDHCGIESEVAGIPR	3	0.9996	4
						HYGYNYSVSNSEK	2	0.9995	1
						HYGYNYSVSNSEKDIMAEIYK	3	0.9618	3
						ICEPGYSPTYQDK	2	0.9968	2
						ILGWGVNGTTPYVLVANSWNTDWDGNGFFK	3	0.9932	1
						KGLVSGGLYSHVGCRRPY	3	0.8831	1
						NGPVEGAFSYSDFLYK	2	0.9997	8
						NGPVEGAFSYSDFLYK	3	0.9995	2
						SGVYQHYVTGEMMGHHAIR	2	0.9997	1
						SGVYQHYVTGEMMGHHAIR	3	0.9994	1

						VLVANSWNTDWDNGFFK	2	0.9898	1
Q5623-1	P07900	HS90A_HUMAN	HSP90AA1	Heat shock protein HSP 90-alpha	1.0000	47.68	36	44	102
Q5623-2	P07900-2	HS90A_HUMAN	HSP90AA1	Isoform 2 of Heat shock protein HSP 90-alpha	1.0000	40.87	36	44	102
						ADLNNLGTIAK	2	0.9997	4
						CIVTSTYGTANMER	2	0.9975	3
						DILNNLGTIAK	2	0.9414	1
						DLVLLVFETALLSGFSLDQPTHANR	3	0.9996	3
						DNSTMGVMAAK	2	0.9952	1
						EGLELPDEEEK	2	0.9954	1
						EGLELPDEEEKK	2	0.9869	2
						EGLELPDEEEKKK	2	0.9921	2
						ELHINLIPNKQDR	2	0.9986	2
						ELISSDALKD	2	0.9989	3
						ELISSDALKIR	2	0.9995	2
						GVGFYSAYLVAEK	2	0.9454	1
						GVVDSDDLNLISR	2	0.9995	5
						HFSVEGQLEFR	2	0.9997	4
						HFSVEGQLEFR	3	0.9992	2
						HGLEVYMIPIEDYCVQQL	2	0.9598	1
						HGLEVYMIPIEDYCVQQLK	3	0.9996	3
						HGLEVYMIPIEDYCVQQLKEFEKG	3	0.9981	4
						HIYYITGETK	2	0.9993	3
						HIYYITGETK	3	0.9411	1
						HIYYITGETKDVANSFAVER	3	0.9994	4
						HLEINPDHSIETLR	2	0.9996	2
						HLEINPDHSIETLR	3	0.9995	4
						HNDDEQYAWESSAGGSF	2	0.9972	2
						HNDDEQYAWESSAGGSFTVR	2	0.9997	3
						HNDDEQYAWESSAGGSFTVR	3	0.996	3
						IPIEDYCVQQLK	2	0.9809	2
						KHGLEVYMIPIEDYCVQQLK	3	0.9995	2
						KHGLEVYMIPIEDYCVQQLK	4	0.9973	2
						KTFENLCK	2	0.9838	1
						LVTSPCCVSTYGTANMER	2	0.9997	2
						LVTSPCCVSTYGTANMER	3	0.9984	5
						NPDDITNEEGEYFK	2	0.9997	4
						SLTNWEDHLAVK	2	0.9997	3
						SLTNWEDHLAVK	3	0.9332	1
						TLTLVDTGIGMTK	2	0.9995	4
						TLVSVTK	2	0.9267	1
						VFIMDNCELUPEYLFIR	3	0.9689	1
						VILHLKEDQTEYLEER	3	0.9919	3
						VILHLKEDQTEYLEERR	3	0.9877	1
						VILHLKEDQTEYLEERR	4	0.882	1
						YIDQELNK	2	0.9678	1
						YMIPIEDYCVQQLK	2	0.9588	1
						YVTSASGDEMVSLEK	2	0.9996	1
Q5624-1	P07911-3	UROM_HUMAN	UMOD	Isoform 3 of Uromodulin	1.0000	15.38	10	10	29
						CPHTRDSTIQVVENGESSQGR	3	0.8523	1
						DSTIQVVENGESSQGR	2	0.9997	4
						FSVQMFRR	2	0.9994	2
						INFACSYPLDMK	2	0.9968	1
						SLGFDKVFMYLSDSR	3	0.9956	2
						STEYGGYACDIDL	2	0.9997	10
						TLDEYWR	2	0.9993	1
						VFMVYLSDSR	2	0.9995	4
						VGGTGMFTVR	2	0.9994	2
						YFIQDR	2	0.9988	2
Q5625-1	P07911-4	UROM_HUMAN	UMOD	Isoform 4 of Uromodulin	1.0000	28.64	20	20	50
Q5625-2	P07911-5	UROM_HUMAN	UMOD	Isoform 5 of Uromodulin	1.0000	26.3	20	20	50
Q5625-3	P07911	UROM_HUMAN	UMOD	Uromodulin	1.0000	27.66	20	20	50
Q5625-4	X6R8G4	X6R8G4_HUMAN	UMOD	Uromodulin	1.0000	25.69	20	20	50
						ALVCADPCQAH	2	0.8378	1
						CPHTRDSTIQVVENGESSQGR	3	0.8523	1
						DGPCGTVLTR	2	0.9929	1
						DSTIQVVENGESSQGR	2	0.9997	4
						DWVSVVTPAR	2	0.9923	4
						FAGNVDLVVLH	2	0.9642	2
						FAGNVDLVVLHCE	2	0.994	3
						FSVQMFRR	2	0.9994	2
						INFACSYPLDMK	2	0.9968	1
						LADEIIR	2	0.9512	1
						MAETCVPLVR	2	0.9997	1
						SLGFDKVFMYLSDSR	3	0.9956	2
						STEYGGYACDIDL	2	0.9997	10
						STEYGGYACDIDLGRWYR	3	0.9955	3
						TALQPMVSALNIR	2	0.9959	3
						TLDEYWR	2	0.9993	1
						TLVLADEIIR	2	0.9752	2
						VFMVYLSDSR	2	0.9995	4
						VGGTGMFTVR	2	0.9994	2
						YFIQDR	2	0.9988	2
Q5626-1	P07996	TSP1_HUMAN	THBS1	Thrombospondin-1	1.0000	12.82	11	12	22
						CTSPDGSWK	2	0.9962	2
						DCVGVNTQICNK	2	0.9996	1
						DLQAICGSCDELSSMVLRL	2	0.9989	1
						FTGSPFGQVGHATANK	2	0.9994	2
						FVFGTTPEDILR	2	0.9988	3
						GGVNDNFQGLVQNV	2	0.9994	2
						IEDANLPPVPDQKFDLVDVAVR	3	0.9351	2
						KVTEENKELANER	2	0.9994	2
						KVTEENKELANER	3	0.9954	1
						LCNNPTQFGGK	2	0.9995	1
						LCNNPTQFGGKCGVDVTENQICNK	3	0.9985	4
						TVITLQDSR	2	0.9994	1
Q5627-1	P08134	RHOC_HUMAN	RHOC	Rho-related GTP-binding protein RhoC	1.0000	29.02	6	6	10
Q5627-2	Q5IR08	Q5IR08_HUMAN	RHOC	Rho-related GTP-binding protein RhoC (Fragment)	1.0000	29.79	6	6	10
						EVFEMATR	2	0.8642	1
						HFCPNVPILVGNKK	3	0.9995	2
						ISAFGLYCSAK	2	0.9886	1
						KLVIWGDGACGK	2	0.9964	1
						LVIWGDGACGK	2	0.984	2
						TCLLVFSK	2	0.9996	3
Q5628-1	P08185	CBG_HUMAN	SERPINA6	Corticosteroid-binding globulin	1.0000	8.4	3	3	4
						EENFYDETTVVK	2	0.9657	2
						GTWTQPFDLASTR	2	0.9868	1
Q5629-1	P08237	PFKAM_HUMAN	PFKM	ATP-dependent 6-phosphofructokinase, muscle type	1.0000	2.31	2	2	3
Q5629-2	P08237-3	PFKAM_HUMAN	PFKM	Isoform 3 of ATP-dependent 6-phosphofructokinase, muscle	1.0000	2.12	2	2	3
						TVFLEVMGR	2	0.9965	2
						VTVLGHVQR	2	0.9913	1
Q5630-1	P08238	HS90B_HUMAN	HSP90AB1	Heat shock protein HSP 90-beta	1.0000	48.76	35	43	100
						ADLNNLGTIAK	2	0.9997	4
						AKFENLCK	2	0.996	1
						ALLFIPR	2	0.9986	2
						CIVTSTYGTANMER	2	0.9975	3
						DLVLLVFETALLSGFSLDQPTH	3	0.9771	1
						DLVLLVFETALLSGFSLDQPTHNR	4	0.9975	2
						EDGTFEER	2	0.9547	2
						EGLELPDEEEK	2	0.9954	1
						EGLELPDEEEKK	2	0.9869	2
						EGLELPDEEEKKK	2	0.9921	2
						EQVANSFAVER	2	0.9997	2

						FYEAFSK	2	0.9722	1
						GFEVVMTEPIDECVQQLK	2	0.9997	5
						GFEVVMTEPIDECVQQLK	3	0.9909	2
						GVGFYSYLVAEK	2	0.9454	1
						GVVDSIDIPLNSR	2	0.9922	7
						GVVDSIDIPLNSR	2	0.9995	5
						HFSVEGQLEFR	2	0.9997	4
						HFSVEGQLEFR	3	0.9992	2
						HLEINPDHPVETLR	2	0.9996	2
						HLEINPDHPVETLR	3	0.9996	3
						HNDDEQYAWESSAGGSF	2	0.9972	2
						HNDDEQYAWESSAGGSFTR	2	0.9997	3
						HNDDEQYAWESSAGGSFTR	3	0.996	3
						IDIPNPQER	2	0.9982	1
						KHLEINPDHPVETLR	4	0.9722	1
						LGHEDESTNR	2	0.9997	1
						LVSSPCCIVSTYGTANMER	2	0.9997	2
						LVSSPCCIVSTYGTANMER	3	0.9978	3
						NPDQITQEYGFYK	2	0.9997	4
						PEEVHGGEEVETAFQAEIQLMSLIINTFYSNK	4	0.9936	2
						RGFEVVMTEPIDECVQQLK	3	0.8946	1
						RLSELLR	2	0.9842	1
						SIYYITGESK	2	0.9997	1
						SIYYITGESKEQVANSFVER	3	0.9937	2
						SLTNDWEDHLAVK	2	0.9997	3
						SLTNDWEDHLAVK	3	0.9332	1
						TLTLVDTGIGMTK	2	0.9995	4
						VILHLKEDQTEYLEER	3	0.9919	3
						VILHLKEDQTEYLEERR	3	0.9877	1
						VILHLKEDQTEYLEERR	4	0.882	1
						YHTSQSGDEMTSLSEYVSR	2	0.9997	3
						YHTSQSGDEMTSLSEYVSR	3	0.9995	3
Q5631-1	P08246	ELNE_HUMAN	ELANE	Neutrophil elastase	1.0000	44.59	11	13	29
						AQFVNWDSIIQR	2	0.9693	2
						GGCASGLYPDAFAPVAQFVNWDSIIQR	2	0.9991	1
						GGCASGLYPDAFAPVAQFVNWDSIIQR	3	0.9992	3
						GGHFCGATLIAPNFVMSAAHCVANVNR	3	0.9643	1
						GLIHGASVFR	3	0.8604	1
						LGNGVQCLAMGWLLGR	2	0.999	5
						NWDSIIQR	2	0.891	1
						QAGVCFGDSGLVCNGLIHGASVFR	3	0.9993	9
						RLGNGVQCLAMGWLLGR	3	0.8277	1
						RSNVCTLVR	2	0.9631	1
						SNVCTLVR	2	0.9616	1
						VVLGAHNLGR	2	0.999	2
						VVLGAHNLGR	3	0.9691	1
Q5632-1	P08263	GSTA1_HUMAN	GSTA1	Glutathione S-transferase A1	1.0000	31.08	5	5	14
Q5632-2	P09210	GSTA2_HUMAN	GSTA2	Glutathione S-transferase A2	1.0000	31.08	5	5	14
						ADIHLVELLYVEELSSLSFPLK	3	0.9991	3
						AILNYASK	2	0.9966	1
						SAEDLDKLR	2	0.9879	1
						SHGQDYLGNK	2	0.9955	1
						WLLAAGVEFEK	2	0.9997	8
Q5633-1	P08294	SODE_HUMAN	SOD3	Extracellular superoxide dismutase [Cu-Zn]	1.0000	61.67	16	21	43
						AGLAASLAGPHSIVGR	2	0.9997	3
						AGLAASLAGPHSIVGR	3	0.9994	2
						AIHVHQFGDLSGGSGRPHVPLAVPHQHPGDFGNFAVR	4	0.9785	1
						AVVYHAGEDDLGR	2	0.9997	4
						AVVYHAGEDDLGR	3	0.9994	1
						AVVYHAGEDDLGRGGNQASVENGNAGR	3	0.964	1
						AVVYHAGEDDLGRGGNQASVENGNAGR	3	0.8852	1
						CVVGVCGPGLWER	2	0.9856	2
						DDDGALHAACQVQPSATLDAAPR	3	0.9994	4
						LACCVVGVCGPGLWER	2	0.9997	3
						LACCVVGVCGPGLWER	3	0.9994	2
						LACCVVGVCGPGLWERQ	2	0.823	1
						RDDDGALHAACQVQPSATLDAAPR	3	0.9997	5
						RDDDGALHAACQVQPSATLDAAPR	4	0.8466	1
						RLACCVVGVCGPGLWER	3	0.9991	2
						VTEIWQVIMQR	2	0.9997	3
						VTEIWQVIMQR	3	0.9984	2
						VTGVVLF	2	0.9997	2
						VVHAGEDDLGR	2	0.9224	1
						VVHAGEDDLGR	2	0.9469	1
						YRAGLAASLAGPHSIVGR	3	0.9994	1
Q5634-1	P08311	CATG_HUMAN	CTSG	Cathepsin G	1.0000	34.9	11	11	21
						AQEGLRPGTLCTV	2	0.9649	4
						AQEGLRPGTLCTVAGWGR	3	0.997	1
						AYLQIOSPAGOSR	2	0.9941	3
						CGGFLVR	2	0.9903	1
						IFGSYDPR	2	0.9993	1
						LQIQSPAGOSR	2	0.8015	1
						NNVAHGVSYGK	2	0.9529	2
						NNVAHGVSYGK	2	0.954	1
						NNVPALPR	2	0.9346	1
						TIQNDIMLLQLSR	2	0.9981	3
						VSSFLPWIR	2	0.9992	3
Q5635-1	P08519	APOA_HUMAN	LPA	Apolipoprotein(a)	1.0000	1.65	6	6	11
						CQSWSSMTFHR	2	0.9982	2
						GTYSTTVGR	2	0.9997	2
						NPDAAVAPCYTR	2	0.9995	3
						TPENYPNAGLTENYCR	2	0.9995	1
						TPENYPNAGLTR	2	0.9589	1
						VQDCHYGQGSYR	2	0.9974	2
Q5636-1	P08582	TRFM_HUMAN	MF12	Melanotransferrin	1.0000	13.69	9	9	15
						ADTDGGLFR	2	0.9533	1
						CLAEAGDVAFAVK	2	0.9978	2
						CLVENAGDVAFAVR	2	0.998	2
						LSVMGCDVLK	2	0.9882	1
						SSHVTIDTLK	2	0.9975	2
						TVGWNVPVGYLVESGR	2	0.9994	3
						VPAHAVVVR	2	0.9955	1
						WCVLSTPEIQK	2	0.9348	1
						YYDYSGAFR	2	0.9982	2
Q5637-1	P08582-2	TRFM_HUMAN	MF12	Isoform 2 of Melanotransferrin	1.0000	15.89	4	4	9
						CLAEAGDVAFAVK	2	0.9978	2
						SSHVTIDTLK	2	0.9975	2
						TVGWNVPVGYLVESGR	2	0.9994	3
						YYDYSGAFR	2	0.9982	2
Q5638-1	P08603	CFAH_HUMAN	CFH	Complement factor H	0.9999	1.95	2	2	2
						CFEGFGIDGPAIAK	2	0.9973	1
						LSYTCGGFR	2	0.9621	1
Q5639-1	P08697	AZAP_HUMAN	SERPINF2	Alpha-2-antiplasmin	1.0000	36.05	16	16	33
Q5639-2	P08697-2	AZAP_HUMAN	SERPINF2	Isoform 2 of Alpha-2-antiplasmin	1.0000	41.45	16	16	33
						DTTGLPLFVGSVR	2	0.8528	1
						FIFEDTTGLPLFVGSVR	2	0.9724	1
						GISEQSLSVGVQHSQSTLESEVGEAAATSIAMSR	3	0.9996	4
						HQMDLVATLSQGLQEL	2	0.9831	2
						FEDTTGLPLFVGSVR	2	0.9863	3
						IQEFLSLPDTVILLNAHFQGFWR	3	0.9848	2
						LCQDLGPGAFR	2	0.9994	3
						LCQDLGPGAFRL	2	0.9681	1
						LQQVLHAGSGPCPLHLR	3	0.9985	4

						MSLSFSVNRPF	2	0.8588	1
						MSLSFSVNRPLF	2	0.8699	1
						MSLSFSVNRPLFF	2	0.9439	1
						MSLSFSVNRPLFFIEDTTGLPLFVGSVR	3	0.9873	1
						NKFDPSLTQR	2	0.8812	1
						SQLGLQELFQAPDLR	2	0.9917	2
						WFLLEQPEIQVAFPFK	3	0.9984	5
Q5640-1	P08727	K1C19_HUMAN	KRT19	Keratin, type I cytoskeletal 19	1.0000	61.25	23	28	56
						AALEDTLAETEAR	2	0.9997	4
						ALEAANGELEVK	2	0.9991	2
						DAEAWFTSR	2	0.9997	2
						DKILGATIENSR	2	0.9994	2
						DVSHYTTIQDLR	2	0.9997	3
						DVSHYTTIQDLR	3	0.9987	1
						EVAGHTEQLQMSR	2	0.9996	2
						FGAQLAHQIALISGIEAQLGDVR	3	0.9997	3
						FGPGVAFR	2	0.9986	1
						GQVGGQSVSEVDSAPGTDLAK	2	0.9997	3
						ILGATIENSR	2	0.999	2
						IVLQIDNAR	2	0.9996	2
						KDAEAWFTSR	2	0.9817	1
						KNHEEEISTLR	2	0.9708	1
						NHEEEISTLR	2	0.9996	1
						QSSATSFSGGLGGGSVR	2	0.9997	2
						SLLEGQEDHYNNLSASK	2	0.9481	1
						SQYEVMAEQNR	2	0.9997	1
						SQYEVMAEQNRK	2	0.9995	2
						SRLEQEIATYR	2	0.9986	2
						TDLEMQIEGLKEELAYLK	2	0.9988	3
						TDLEMQIEGLKEELAYLK	3	0.9986	3
						TDLEMQIEGLKEELAYLKK	3	0.9991	2
						TDLEMQIEGLKEELAYLKK	4	0.9867	1
						TKFETEQLR	2	0.9992	2
						TKFETEQLR	3	0.9955	1
						TLQGLEIELOSLSMK	2	0.9997	2
						TLQGLEIELOSLSMK	3	0.9996	4
Q5641-1	P08729	K2C7_HUMAN	KRT7	Keratin, type II cytoskeletal 7	1.0000	56.08	30	37	79
						AAEAWYQTK	2	0.9988	3
						AAEAWYQTKFETLQAQAGK	3	0.9807	2
						AKLEAAIAEAER	2	0.9987	2
						AKLEAAIAEAER	3	0.9967	1
						AKLEAAIAEAERGELALK	3	0.9923	2
						AKQELEAALQR	2	0.9981	2
						AKQELEAALQR	3	0.9927	1
						AQKEEMAK	2	0.9037	1
						DVDAAVMSKVELEAK	2	0.9994	2
						ELQSQISDTSVLSMDNSR	2	0.9997	2
						EVTINQSLAPLR	2	0.998	2
						EVTINQSLAPLRDADPSLQR	3	0.9241	1
						EYQELMSVK	2	0.9703	1
						FETLQAQAGK	2	0.9937	1
						GQLEALQVDGGR	2	0.9997	3
						GQLEALQVDGGRLEAELR	2	0.9985	3
						GQLEALQVDGGRLEAELR	3	0.9995	4
						KLLEGEESR	2	0.9986	2
						LALDIEATYRK	2	0.9972	1
						LEAAIAEAER	2	0.9828	2
						LPDIFEAQIAGLR	2	0.9998	5
						LPDIFEAQIAGLR	3	0.9996	4
						LQAEIDNIK	2	0.9978	1
						LQAEIDNIKNQR	2	0.9989	2
						NTRNEISEMNR	2	0.9857	1
						SLDLGIIAEVK	2	0.9997	5
						SMQDVVEDFK	2	0.9986	1
						SSRLPDIFEAQIAGLR	2	0.999	2
						SSRLPDIFEAQIAGLR	3	0.9995	3
						TAAENEFVLK	2	0.9638	2
						TAAENEFVLKK	2	0.9973	3
						TAAENEFVLKK	3	0.9724	1
						TLNETELQSQISDTSVLSMDNSR	3	0.999	2
						VDALNDEINFLR	2	0.9997	5
						VDALNDEINFLR	3	0.9905	1
						VELEAKVDALNDEINFLR	3	0.9716	2
						WTLQEQK	2	0.9882	1
Q5642-1	P63096	GNAI1_HUMAN	GNAI1	Guanine nucleotide-binding protein G(i) subunit alpha-1	1.0000	11.02	3	4	6
Q5642-2	P08754	GNAI3_HUMAN	GNAI3	Guanine nucleotide-binding protein G(k) subunit alpha	1.0000	11.02	3	4	6
						EYTHFTCATDTK	2	0.9958	2
						LLLLGAGESGK	2	0.958	1
						NVQFVDAVTDVIK	2	0.9937	1
						NVQFVDAVTDVIK	3	0.9912	2
Q5643-1	P08779	K1C16_HUMAN	KRT16	Keratin, type I cytoskeletal 16	1.0000	59.62	25	31	59
						APSYGGGGLVSSR	2	0.9995	3
						ASLENSLEETK	2	0.9996	1
						ASLENSLEETKGR	2	0.9933	1
						CEMEQSQSQEYQILLDVK	2	0.9996	2
						CEMEQSQSQEYQILLDVK	3	0.997	3
						DAETWFLSK	2	0.9982	2
						DAETWFLSKTEELNKEVASSELVQSSR	3	0.9953	2
						EVASSELVQSSR	2	0.9996	1
						EVFTSSSSSSSR	2	0.9983	2
						GQTGGDVNVEMDAAPGVOLSR	2	0.9997	2
						GSCGGGGGGSSSR	2	0.9993	1
						IIAATIENAQPILOIDNAR	2	0.9997	2
						IIAATIENAQPILOIDNAR	3	0.9996	3
						ILNEMMDQVEQMAEK	2	0.9972	2
						ISSVLAGGSCR	2	0.9994	1
						LLEGEDAHLLSQSQASGQS	2	0.9948	2
						LLEGEDAHLLSQSQASGQSSSR	3	0.9996	3
						NHEEMLALR	2	0.9571	2
						NKIIAATIENAQPILOIDNAR	3	0.9982	2
						QRPSEIKDYSPIYK	3	0.814	1
						RLLEGEDAHLLSQSQASGQSSSR	2	0.8349	1
						RLLEGEDAHLLSQSQASGQSSSR	3	0.9992	2
						TDLEMQIEGLKEELAYLR	2	0.9982	2
						TDLEMQIEGLKEELAYLR	3	0.9994	3
						TDLEMQIEGLKEELAYLRK	3	0.9976	2
						TEELNKEVASSELVQSSR	3	0.9973	1
						TYEHELALR	2	0.9809	2
						TYEHELALR	3	0.8301	1
						VLQGLEIELOSLSMK	2	0.9801	1
						VLQGLEIELOSLSMK	3	0.9935	3
						YCMQLSQIQLIGLSVEEQLAQLR	3	0.9994	3
Q5644-1	P09211	GSTP1_HUMAN	GSTP1	Glutathione S-transferase P	1.0000	46.19	8	8	19
						ALPGQLKPFETLLSQNGGK	3	0.9972	2
						ASCLYGQLPK	2	0.9996	3
						FQDGLDLTYQSNTILR	2	0.9997	6
						MLIADQGSQWKEEVTVTWEQESLK	3	0.9921	2
						PPYTVVYFVR	2	0.9984	3
						SCYHGQLPK	2	0.9983	1
						YISLYTNYEAGK	2	0.9416	1
						YISLYTNYEAGKD	2	0.8939	1
Q5645-1	P09429	HMG81_HUMAN	HMG81	High mobility group protein B1	1.0000	14.88	5	6	13
Q5645-2	Q577C4	Q577C4_HUMAN	HMG81	High mobility group protein B1	1.0000	20.25	5	6	13

Q5645-3	Q5T7C6	Q5T7C6_HUMAN	HMG81	High mobility group protein B1 (Fragment)	1.0000	19.75	5	6	13
						GEHPGLSIGDVAK	2	0.9879	2
						IKGEHPGLSIGDVAK	2	0.9992	3
						IKGEHPGLSIGDVAK	3	0.9984	2
						IKGEHPGLSIGDVAKK	3	0.9578	1
						RPPSAFLF	2	0.8304	1
						RPPSAFLFCEYRPK	3	0.9987	4
Q5646-1	P09525	ANXA4_HUMAN	ANXA4	Annexin A4	1.0000	13.48	3	7	11
						GAGTDEGLIEILASR	2	0.9997	2
						GLGTDEDAISVLAYR	2	0.9997	5
						GLGTDEDAISVLAYR	3	0.9986	3
						ISQTYQQQVGR	2	0.9993	1
Q5647-1	P09758	TACD2_HUMAN	TACSD2	Tumor-associated calcium signal transducer 2	1.0000	13.62	3	3	6
						AAGDVIDGDAAYFER	2	0.9997	2
						ALGSGMAVDCSTLTK	2	0.9995	3
						MTVCSPDGPGR	2	0.9908	1
Q5648-1	P09871	C15_HUMAN	C15	Complement C1s subcomponent	1.0000	16.28	8	8	17
						CVPCVGVPR	2	0.8785	1
						DVVGITCLDGFVVEGR	2	0.9995	4
						GFOVVTLR	2	0.9993	3
						LPVAPLR	2	0.972	1
						QFGPYCGHFPPLNIETK	3	0.9533	1
						SNALDIFQDILTGQK	2	0.9878	2
						SSNNPHSPIVEEFQVPYNYK	3	0.8922	2
						SWDIEVPEGGIHLFY	2	0.9818	3
Q5649-1	P09960-2	LKHA4_HUMAN	LTA4H	Isoform 2 of Leukotriene A-4 hydrolase	0.9995	3.57	2	2	3
Q5649-2	P09960	LKHA4_HUMAN	LTA4H	Leukotriene A-4 hydrolase	0.9995	3.11	2	2	3
						CSVDFTR	2	0.9572	1
						LIALVGALESR	2	0.9807	2
Q5650-1	P0C0L4	CD4A_HUMAN	C4A	Complement C4-A	1.0000	32.45	56	62	150
						AACAQLNDFLQEYGTGCGQV	2	0.9997	4
						ADGSYAAWLSR	2	0.992	2
						AFFQDALEK	2	0.972	1
						AEMADQAAWLTR	2	0.9985	3
						ALDALSAYWASHTTEER	2	0.9905	2
						ALSAYWASHTTEER	2	0.9519	2
						ASAGLLGAHAAITAYALTLTK	2	0.9997	2
						ASAGLLGAHAAITAYALTLTK	3	0.9995	3
						AVGSGATFSHYYY	2	0.9477	1
						AYWASHTTEER	2	0.9874	3
						CSVFGAPSK	2	0.9985	2
						DALSAYWASHTTEER	2	0.9929	4
						DHAVDLIQK	2	0.9992	1
						GSSTWLTAFYVK	2	0.9994	5
						ECVGFQVQVPGVLQVQASATLYDYNNPER	3	0.9734	1
						ECVGFQVQVPGVLQVQASATLYDYNNPERR	3	0.9997	3
						EFHLHLR	2	0.899	1
						EGAIHREELVYELNPLDHR	3	0.9984	4
						FACYVPR	2	0.9663	1
						FGLLDEGKK	2	0.9982	2
						GLCVATPVQLR	2	0.9591	1
						GLEEELQF	2	0.8724	1
						GLEEELQFSLGSK	2	0.9997	5
						GLODEGYR	2	0.9763	2
						GSFEPPVGDAVSK	2	0.9995	7
						HLVPGAPFLQ	2	0.8824	1
						HLVPGAPFLQALVR	2	0.9751	1
						HLVPGAPFLQALVR	3	0.9997	5
						KADGSYAAWLSR	2	0.9994	4
						KADGSYAAWLSR	3	0.9991	4
						KYVLPNFEVK	2	0.8029	1
						KYVLPNFEVK	3	0.9942	1
						LGQYASPTAK	2	0.9992	1
						LHLETDSLALVALGALDTALYAAGSK	3	0.9994	3
						LLATLCSAEVCQCAEGK	2	0.9992	3
						LLHHEGK	2	0.8616	1
						LNMGITDLQGLR	2	0.9901	1
						PVAFSVVPTAAAVSLK	2	0.9861	2
						QGSFGGFR	2	0.9945	1
						SAYWASHTTEER	2	0.9807	2
						SFFFNWMLWR	2	0.9994	5
						SHALQLNNR	2	0.9995	4
						STQDTVIALDALSAYWASH	2	0.8476	1
						STQDTVIALDALSAYWASHTTEER	3	0.9995	5
						TAYALTLTK	2	0.952	1
						TTNIQGINLLFSSR	2	0.9995	3
						TYNVLDKM	2	0.8476	1
						VDFTLSER	2	0.9983	1
						VEYFQVK	2	0.998	1
						VGDTNLNLNR	2	0.9988	3
						VGLSGMAIADVTLLSGFHALR	3	0.9996	4
						VHYTVCIWR	2	0.9994	2
						VHYTVCIWR	3	0.9969	2
						VLSLAQEQVGGSPK	2	0.9997	2
						VLSLAQEQVGGSPKEL	2	0.9811	2
						VTASDPLDITLGSAGLSPGGVASLLR	2	0.9997	4
						VTASDPLDITLGSAGLSPGGVASLLR	3	0.9989	4
						WASHTTEER	2	0.9957	1
						YIYKPVQGVAY	2	0.8997	1
						YIYKPVQGVAYVR	3	0.9987	2
						YVSHFETEGPHVLLYFDSVPTSR	3	0.9996	5
						YWASHTTEER	2	0.949	2
Q5651-1	P0C0L5	CD4B_HUMAN	C4B	Complement C4-B	1.0000	31.48	55	60	145
						AACAQLNDFLQEYGTGCGQV	2	0.9997	4
						ADGSYAAWLSR	2	0.992	2
						AFFQDALEK	2	0.972	1
						AEMADQAAWLTR	2	0.9994	2
						ALDALSAYWASHTTEER	2	0.9905	2
						ALSAYWASHTTEER	2	0.9519	2
						ASAGLLGAHAAITAYALTLTK	2	0.9997	2
						ASAGLLGAHAAITAYALTLTK	3	0.9995	3
						AVGSGATFSHYYY	2	0.9477	1
						AYWASHTTEER	2	0.9874	3
						CSVFGAPSK	2	0.9985	2
						DALSAYWASHTTEER	2	0.9929	4
						DHAVDLIQK	2	0.9992	1
						ECVGFQVQVPGVLQVQASATLYDYNNPER	3	0.9734	1
						ECVGFQVQVPGVLQVQASATLYDYNNPERR	3	0.9997	3
						EFHLHLR	2	0.899	1
						EGAIHREELVYELNPLDHR	3	0.9984	4
						FACYVPR	2	0.9663	1
						FGLLDEGKK	2	0.9982	2
						GLCVATPVQLR	2	0.9591	1
						GLEEELQF	2	0.8724	1
						GLEEELQFSLGSK	2	0.9997	5
						GLODEGYR	2	0.9763	2
						GSFEPPVGDAVSK	2	0.9995	7
						GSSTWLTAFYVK	2	0.9995	4
						HLVPGAPFLQ	2	0.8824	1
						HLVPGAPFLQALVR	2	0.9751	1
						HLVPGAPFLQALVR	3	0.9997	5
						KADGSYAAWLSR	2	0.9994	4
						KADGSYAAWLSR	3	0.9991	4

						KYVLPNFEVK	3	0.9942	1
						LGQYASPTAK	2	0.9992	1
						LHLETOSLALVALGALDTALYAAGSK	3	0.9994	3
						LLATLCSAEVCCQCAEGK	2	0.9992	3
						LLHHEGK	2	0.8616	1
						LNMGITDLQGLR	2	0.9901	1
						QGSFQSGGR	2	0.9945	1
						SAYWASHHTTEER	2	0.9807	2
						SFFPENWLWR	2	0.9994	5
						SHALQLNRR	2	0.9995	4
						STQDTVIALDALSAYWASH	2	0.8476	1
						STQDTVIALDALSAYWASHHTTEER	3	0.9995	5
						TAYALTTLK	2	0.952	1
						TTNIQGINLLFSSR	2	0.9995	3
						TYNVLDOMK	2	0.8476	1
						VDFTLSER	2	0.9983	1
						VEYGFQVK	2	0.998	1
						VGOTLNINLR	2	0.9988	3
						VLSGMAIADVTLLSGFHAI	3	0.9996	4
						YHYTVCIWR	2	0.9994	2
						YHYTVCIWR	3	0.9969	2
						VLSAQEQVGGSPK	2	0.9997	2
						VLSAQEQVGGSPK	2	0.9811	2
						VTASDPLDTLGSSEALSPGGVASLLR	2	0.9997	4
						VTASDPLDTLGSSEALSPGGVASLLR	3	0.9989	4
						WIASHTTEER	2	0.9957	1
						YIYGKPVQGVAY	2	0.8997	1
						YIYGKPVQGVAY	3	0.9987	2
						YVSHFETEGPHVLLYFDSVPTSR	3	0.9996	5
						YWIASHTTEER	2	0.949	2
Q5652-1	POCG04	LAC1_HUMAN	IGLC1	Ig lambda-1 chain C regions	1.0000	17.17	4	4	13
						ATLVCLISDFYFGAVTVAWK	3	0.9997	5
						SYSQVTHEGSTVE	2	0.9852	2
						SYSQVTHEGSTVEK	2	0.9997	2
						YAASSYLSLTPQWK	2	0.9997	4
Q5653-1	POCG05	LAC2_HUMAN	IGLC2	Ig lambda-2 chain C regions	1.0000	65.09	8	10	30
Q5653-2	POCG06	LAC3_HUMAN	IGLC3	Ig lambda-3 chain C regions	1.0000	65.09	8	10	30
						AAPSVTLFPSSEELQANK	2	0.9996	8
						ATLVCLISDFYFGAVTVAWK	2	0.9435	1
						ATLVCLISDFYFGAVTVAWK	2	0.9997	4
						ATLVCLISDFYFGAVTVAWK	3	0.9997	5
						SYLSLTPQWK	2	0.896	1
						SYSQVTHEGSTV	2	0.9899	2
						SYSQVTHEGSTVE	2	0.9852	2
						SYSQVTHEGSTVEK	2	0.9997	2
						YAASSYLSLTPQWK	2	0.9997	4
						YAASSYLSLTPQWK	3	0.9964	1
Q5654-1	PODMED	SETLP_HUMAN	SETSIP	Protein SETSIP	1.0000	16.56	5	5	14
						EFHLESQDPSK	2	0.9994	2
						IDFYDENPFYENK	2	0.9997	3
						LQPPFFQKR	3	0.9708	1
						SGYRIDFYDENPFYENK	3	0.9971	4
						VEVTEFEDIK	2	0.9997	4
Q5655-1	P10153	RNAS2_HUMAN	RNASE2	Non-secretory ribonuclease	1.0000	29.81	6	10	23
						DPPQYVPVPHLDR	2	0.9958	3
						DPPQYVPVPHLDR	3	0.9995	2
						DPPQYVPVPHLDR	3	0.9334	1
						NONTELTTFANVV	2	0.8368	1
						RDPQYVPVPHLDR	2	0.9996	3
						RDPQYVPVPHLDR	3	0.9997	4
						RDPQYVPVPHLDR	4	0.999	1
						RDPQYVPVPHLDR	3	0.9993	2
						YAQTANMFYVACDNR	2	0.9997	4
						YAQTANMFYVACDNR	3	0.9996	2
Q5656-1	P10253	LYAG_HUMAN	GAA	Lysosomal alpha-glucosidase	0.9954	2	2	2	2
						FDCAPDK	2	0.9468	1
						VTSEGAGLQLOK	2	0.9141	1
Q5657-1	P10451-2	OSTP_HUMAN	SPP1	Isoform B of Osteopontin	1.0000	12.67	4	4	30
						AIPVAQDLNAPSOWDSR	2	0.9997	22
						GDSVYGLR	2	0.9997	3
						LNAPSOWDSR	2	0.9849	3
						QNLLAPETLPSK	2	0.9989	2
Q5658-1	P10451-5	OSTP_HUMAN	SPP1	Isoform 5 of Osteopontin	1.0000	38.67	22	22	68
						AIPVAQDLNAPSD	2	0.9702	1
						AIPVAQDLNAPSOWDSR	2	0.9997	22
						AVATWLNPDPSQK	2	0.9969	3
						DLNAPSOWDSR	2	0.8173	1
						EHSVDVDSQELSK	2	0.8529	1
						FRISHELDSASSEVN	2	0.935	2
						GDSVYGLR	2	0.9997	3
						GKDSYETSQLDQDSAEHSHK	2	0.9872	2
						GKDSYETSQLDQDSAEHSHK	2	0.9996	3
						GKDSYETSQLDQDSAEHSHKQ	3	0.9135	1
						IPVAQDLNAPSOWDSR	2	0.9971	2
						ISHELDSASSEVN	2	0.9996	4
						KANDESHSDVIDSQELSK	2	0.9997	2
						LNAPSOWDSR	2	0.9849	3
						PDVATWLNPDPSQK	2	0.9943	3
						QLYNKYPDVATWLN	2	0.8152	1
						QLYNKYPDVATWLNPDPS	2	0.8754	1
						QLYNKYPDVATWLNPDPSQ	2	0.8621	1
						QNLLAPQTLPSK	2	0.9997	2
						VAQDLNAPSOWDSR	2	0.9936	2
						WLNPDPSQK	2	0.9731	1
						YPDVATWLNPDPSQK	2	0.9995	7
Q5659-1	P10451-4	OSTP_HUMAN	SPP1	Isoform D of Osteopontin	1.0000	17.81	6	6	31
Q5659-2	P10451	OSTP_HUMAN	SPP1	Osteopontin	1.0000	16.56	6	6	31
						AIPVAQDLNAPSOWDSR	2	0.9997	22
						AVSSEETNDFKQETLPSK	2	0.9481	1
						GDSVYGLR	2	0.9997	3
						LNAPSOWDSR	2	0.9849	3
						QNLLAPQNAVSEETNDFK	2	0.9924	1
						QNLLAPQNAVSEETNDFKQETLPSK	3	0.9823	1
Q5660-1	P10643	CO7_HUMAN	C7	Complement component C7	0.9601	2.37	1	1	2
						LIDQYGYHLYQSGSLGGEYR	3	0.9601	2
Q5661-1	P10809	CH60_HUMAN	HSPD1	60 kDa heat shock protein, mitochondrial	1.0000	11.52	6	6	7
						AAVEGELGGGCALLR	2	0.9989	2
						CEFQDAYVLLSEK	2	0.9991	1
						IGIEIKR	2	0.9735	1
						NAGVEGSLVEK	2	0.9777	1
						RGVMLAVDAVIAELK	3	0.9982	1
						RGVMLAVDAVIAELKK	3	0.9335	1
Q5662-1	P10909-2	CLUS_HUMAN	CLU	Isoform 2 of Clusterin	1.0000	22.75	18	23	47
						ASSIDELFQDR	2	0.9996	5
						ASSIDELFQDR	3	0.9865	1
						ASSIDELFQDRF	2	0.9828	2
						CREILSDCSTNNPSQ	2	0.9379	2
						CREILSDCSTNNPSQAK	3	0.996	1
						DQTVSDNELQEMSGSSK	2	0.9979	2
						EILSDCSTNNPSQ	2	0.9832	4
						EILSDCSTNNPSQA	2	0.9688	1
						EILSDCSTNNPSQAK	2	0.9997	4
						ELDESQVAER	2	0.9995	3

						KTLSNLEAK	2	0.9968	1
						KTLSNLEAK	3	0.9756	1
						KTLSNLEAKK	2	0.9974	1
						KTLSNLEAKK	3	0.9774	1
						LF0SDPITVTPVEVSR	2	0.9997	3
						RELDESQVAER	2	0.9995	3
						RELDESQVAER	3	0.9956	1
						RVTTVASHTSDSDVPSGVTEVVVK	3	0.8416	1
						VPSGVTEVVVK	2	0.9664	1
						VTTVASHTSDSDVPSG	2	0.9935	2
						VTTVASHTSDSDVPSG	2	0.9935	2
						VTTVASHTSDSDVPSG	2	0.8882	2
						VTTVASHTSDSDVPSGVTEVVVK	2	0.9996	2
						VTTVASHTSDSDVPSGVTEVVVK	3	0.9991	3
Q5663-1	P10909	CLUS_HUMAN	CLU	Clusterin	1.0000	18.04	10	11	30
Q5663-2	P10909-3	CLUS_HUMAN	CLU	Isoform 3 of Clusterin	1.0000	29.56	10	11	30
Q5663-3	P10909-4	CLUS_HUMAN	CLU	Isoform 4 of Clusterin	1.0000	19.47	10	11	30
Q5663-4	P10909-5	CLUS_HUMAN	CLU	Isoform 5 of Clusterin	1.0000	17.61	10	11	30
						ASSIDELFQDR	2	0.9996	5
						EILSVDCSTNNPSQ	2	0.9832	4
						EILSVDCSTNNPSQAK	2	0.9997	4
						ELDESQVAER	2	0.9995	3
						LF0SDPITVTPVEVSR	2	0.9997	3
						RELDESQVAER	2	0.9995	3
						RELDESQVAER	3	0.9956	1
						RVTTVASHTSDSDVPSGVTEVVVK	3	0.8416	1
						VPSGVTEVVVK	2	0.9664	1
						VTTVASHTSDSDVPSG	2	0.9935	2
						VTTVASHTSDSDVPSGVTEVVVK	3	0.9991	3
Q5664-1	P11021	GRP78_HUMAN	HSPA5	78 kDa glucose-regulated protein	1.0000	14.98	8	9	18
						AKFEELNMDLFR	2	0.9763	2
						AKFEELNMDLFR	3	0.9925	2
						IIIESPYEGEDPSKTLR	2	0.9997	3
						IIIEPTAAAIAYGLDK	2	0.9947	2
						IIIEPTAAAIAYGLDKR	3	0.9632	1
						ITPSYVAFTEGER	2	0.9991	2
						TFAPEISAMVLTK	2	0.9988	2
						TWNDPVQQDIK	2	0.9994	2
						VEIANDQGNR	2	0.9988	2
Q5665-1	P11047	LAMC1_HUMAN	LAMC1	Laminin subunit gamma-1	1.0000	3.73	4	4	4
						EAQQALGSAADATEAK	2	0.9984	1
						NTIETGNLAEQAR	2	0.9535	1
						SQECYFDPPELYR	2	0.9854	1
						TFAEYTDLDNEVNNMLK	2	0.9923	1
Q5666-1	P11215	ITAM_HUMAN	ITGAM	Integrin alpha-M	0.9982	0.87	1	1	2
Q5666-2	P11215-2	ITAM_HUMAN	ITGAM	Isoform 2 of Integrin alpha-M	0.9982	0.87	1	1	2
						YVIGQDAFR	2	0.9708	2
Q5667-1	P11216	PYGB_HUMAN	PYGB	Glycogen phosphorylase, brain form	0.9712	1.9	1	1	1
						LQDFNVGDYIEAVLDR	2	0.9712	1
Q5668-1	P11678	PERE_HUMAN	EPX	Eosinophil peroxidase	1.0000	10.63	7	7	11
						DFLPLVLGK	2	0.9929	1
						FCGLSQPR	2	0.9789	1
						IICONTGITTVSR	2	0.9986	2
						IPCFLAGDTR	2	0.9975	2
						IVYEGGIDPILR	2	0.9978	2
						VANVFTLAFR	2	0.9994	2
						VGPLLCLEFNGFR	2	0.9935	1
Q5669-1	P12109	CO6A1_HUMAN	COL6A1	Collagen alpha-1(VI) chain	1.0000	2.33	2	2	2
						TAEYDVAGESHFR	3	0.99	1
						VPSYQALLR	2	0.9801	1
						0.45	1	1	2
						AEVDVVIQVR	2	0.9721	2
Q5670-1	P12259	FAS_HUMAN	F5	Coagulation factor V	0.9845	15.07	2	2	3
						FYTIELKVE	2	0.9654	1
						TVQIAAVDVIR	2	0.9967	2
Q5671-1	P12273	PIP_HUMAN	PIP	Prolactin-inducible protein	0.9999	17.06	5	5	7
						FCTGLTQIETLFK	2	0.9996	2
						LAVALSSLDGDLGR	2	0.9559	1
						LGFEVELVQMVDGVK	2	0.9994	2
						LLIEMQQR	2	0.9478	1
						VLTRELVAELR	2	0.9896	1
Q5673-1	P12724	ECP_HUMAN	RNA5E3	Eosinophil cationic protein	1.0000	36.88	13	15	40
						ANVNVNCGNQSR	2	0.9884	1
						AQWFAIQHI	2	0.9967	2
						AQWFAIQHISLNPPR	2	0.9996	6
						AQWFAIQHISLNPPR	3	0.9995	5
						DSPRPVVPVHLDTTI	2	0.9969	2
						FANVNVNCGNQSR	2	0.9459	2
						FYVVACDNR	2	0.9996	1
						FYVVACDNRD	2	0.9521	3
						FYVVACDNRDP	3	0.9952	2
						NVNVNCGNQSR	2	0.9695	2
						TFANVNVNCGNQSR	2	0.9896	4
						TFANVNVNCGNQSR	3	0.9983	2
						YPVVPVHL	2	0.9381	1
						YPVVPVHLD	2	0.9846	1
						YPVVPVHLDTTI	2	0.9996	6
Q5674-1	Q9UII8	Q9UII8_HUMAN	CDH1	Cadherin 1, type 1, E-cadherin (Epithelial), isoform CRA_c	0.9993	4.63	2	2	2
Q5674-2	P12830	CADH1_HUMAN	CDH1	Cadherin-1	0.9993	4.31	2	2	2
						DTANWLEINPOTGAISTR	2	0.9919	1
						YLRPANPDEIGNFIDENLK	3	0.9191	1
Q5675-1	P12838	DEF4_HUMAN	DEFA4	Neutrophil defensin 4	1.0000	17.53	2	2	7
						VGNCLIGVSFTY	2	0.8337	1
						VGNCLIGGVSFYCCCTR	2	0.9995	6
Q5676-1	P12931-2	SRC_HUMAN	SRC	Isoform 2 of Proto-oncogene tyrosine-protein kinase Src	0.9325	3.69	1	1	1
Q5676-2	P12931	SRC_HUMAN	SRC	Proto-oncogene tyrosine-protein kinase Src	0.9325	3.73	1	1	1
						AGPLAGGVTTVALYDYESR	2	0.9325	1
Q5677-1	P12955-2	PEPD_HUMAN	PEPD	Isoform 2 of Xaa-Pro dipeptidase	0.9750	4.42	1	1	1
Q5677-2	P12955-3	PEPD_HUMAN	PEPD	Isoform 3 of Xaa-Pro dipeptidase	0.9750	4.66	1	1	1
Q5677-3	P12955	PEPD_HUMAN	PEPD	Xaa-Pro dipeptidase	0.9750	4.06	1	1	1
						IEEDVVVDSGIELTTCVPR	2	0.975	1
Q5678-1	P12956	XRCC6_HUMAN	XRCC6	X-ray repair cross-complementing protein 6	1.0000	6.57	3	3	4
						DIISIAEDEDLR	2	0.983	1
						NIYVQLQELDNGAK	2	0.9997	2
						SDSFENPVLQHFRR	2	0.9987	1
Q5679-1	P13639	EF2_HUMAN	EEF2	Elongation factor 2	1.0000	30.65	18	22	43
						AGIIASAR	2	0.9828	1
						ALLEQLQPELVQTFQR	2	0.9997	3
						ALLEQLQPELVQTFQR	3	0.9996	3
						AYLPVNESFGFTADLR	2	0.9997	2
						AYLPVNESFGFTADLR	3	0.9631	1
						CLYASVLTAGPR	2	0.9993	2
						EGIPALDNFLDKL	2	0.999	2
						ETVSESNVCLSK	2	0.9997	3
						FSVSPVVR	2	0.9615	1
						GEGQLGPAER	2	0.9725	1
						GGGQIPTAR	2	0.9979	1
						GHVFESQVAGTPMFVVK	3	0.8772	1
						GVQVLEIKDSVAGFQWATK	3	0.9813	2
						KWQCGPDGTGPHILDTIK	3	0.9989	3
						STAIISLYELSENLDPIK	2	0.9996	3
						STAIISLYELSENLDPIK	3	0.9988	2
						TFCQLDPIFK	2	0.9993	3
						TGTTTTEHAHNMNR	2	0.9994	1

[illegible]

						NTGICTIGPASR	2	0.9996	3
						PVQEAWAEDVDLR	2	0.9952	3
Q5690-1	P14625	ENPL_HUMAN	HSP90B1	Endoplasmic	1.0000	19.05	12	12	15
						DISTNYYASQKK	2	0.9665	2
						EAESSPFVER	2	0.9977	1
						FAFQAENVNR	2	0.9993	1
						FQSSHHPTDLSLDQYR	3	0.9711	1
						GYEVRLTPVDYEQALPEFDGKR	3	0.9965	1
						KEAESSPFVER	2	0.9834	1
						LGVIDHMSNR	2	0.9979	2
						LIINSLYK	2	0.928	1
						LISLTDENALSGNEELTVK	2	0.9981	1
						NLLHVTDTGVMGTRELVK	3	0.9345	1
						SGTSEFLNK	2	0.9917	1
						SILFVPTSAPR	2	0.9986	2
Q5691-1	P14780	MMP9_HUMAN	MMP9	Matrix metalloproteinase-9	0.9968	4.1	2	2	4
						AFALWSAVTPLTFTFR	2	0.9755	2
						QVWVYTGASVLGPR	2	0.9778	2
Q5692-1	P14868	SYDC_HUMAN	DARS	Aspartate-tRNA ligase, cytoplasmic	1.0000	10.98	5	5	6
Q5692-2	Q68CR9	Q68CR9_HUMAN	DKFZp781B11202	Aspartate-tRNA ligase, cytoplasmic	1.0000	13.72	5	5	6
						ESIVDVEGVVR	2	0.9923	1
						FOTEIQTVMK	2	0.9517	1
						IGSCTQQDVELHVQK	3	0.9871	1
						IYVISLAEP	2	0.9987	2
						VFSIGPVFR	2	0.9542	1
Q5693-1	P14923	PLAK_HUMAN	JUP	Junction plakoglobin	1.0000	7.38	4	4	5
						LNTIPLFVQLLYSSVENIQR	3	0.9877	1
						LVQNCLWTLR	2	0.8793	1
						NEGATYAAAVLFR	2	0.9994	2
Q5694-1	P15121	ALDR_HUMAN	AKR1B1	Aldose reductase	1.0000	42.41	2	0.9635	1
						HIDCAHYQNEVGVQAIQEK	10	10	19
						LDYLDLYLHWPTGFKPGK	3	0.9995	3
						LUQYQSK	3	0.9963	3
						MPILGLGTWK	2	0.9678	1
						MPILGLGTWK	2	0.9869	1
						MPILGLGTWK	2	0.9893	2
						REELFIVSK	2	0.9744	1
						SPPGQVTEAVK	2	0.9987	2
						VAIDGYR	2	0.9996	1
						VCALLSCTSHKDYPPHEEF	3	0.9639	2
						VDFELSSQDMITLLSYNR	2	0.9996	3
Q5695-1	P15153	RAC2_HUMAN	RAC2	Ras-related C3 botulinum toxin substrate 2	1.0000	29.69	5	5	8
						CVVVGDGAVGK	2	0.9993	4
						LRPLSYPTQDVRLICSLSPSPASVENV	3	0.8744	1
						SLVSPASVENV	2	0.9155	1
						TVDFDAIR	2	0.8878	1
						YLECSALTOR	2	0.9867	1
Q5696-1	P18669	PGAM1_HUMAN	PGAM1	Phosphoglycerate mutase 1	1.0000	9.84	2	2	3
Q5696-2	P15259	PGAM2_HUMAN	PGAM2	Phosphoglycerate mutase 2	1.0000	9.88	2	2	3
						ALPFWNEEIVPQIK	2	0.9971	2
						VLIAAHGNSLR	2	0.9987	1
Q5697-1	P15374	UCHL3_HUMAN	UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	0.9993	10.87	2	2	2
						WLPLEANPEVTNQFLK	2	0.993	1
Q5698-1	P15428	PGDH_HUMAN	HPGD	15-hydroxyprostaglandin dehydrogenase [NAD(+)]	1.0000	45.49	2	0.9006	1
						AALDEQFEPQK	10	11	25
						AFAEAALLK	2	0.9997	4
						GIHFQDYDTPFQAK	2	0.9996	2
						HGIVGFTR	2	0.9997	4
						LDILVNNAGVNNK	2	0.9965	2
						SAALANLMSVGR	2	0.9997	2
						TLFIQCDVADQQQLR	2	0.9995	2
						TLFIQCDVADQQQLR	2	0.9997	3
						TLFIQCDVADQQQLR	3	0.9979	2
						VALVDWNLEAGVQCK	2	0.9997	2
						VALVTGAAQIGIR	2	0.9997	1
						VVDHFGR	2	0.9946	1
Q5699-1	P15428-2	PGDH_HUMAN	HPGD	Isoform 2 of 15-hydroxyprostaglandin dehydrogenase [NAD(+)]	1.0000	43.26	7	7	14
						AALDEQFEPQK	2	0.9997	4
						AFAEAALLK	2	0.9996	2
						HGIVGFTR	2	0.9965	2
						LDILVNNAGVNNK	2	0.9997	2
						VALVDWNLEAGVQCK	2	0.9997	2
						VALVTGAAQIGIR	2	0.9997	1
						VVDHFGR	2	0.9946	1
Q5700-1	P15428-5	PGDH_HUMAN	HPGD	Isoform 5 of 15-hydroxyprostaglandin dehydrogenase [NAD(+)]	1.0000	50.51	8	9	22
						AALDEQFEPQK	2	0.9997	4
						AFAEAALLK	2	0.9996	2
						GIHFQDYDTPFQAK	2	0.9997	4
						HGIVGFTR	2	0.9965	2
						SAALANLMSVGR	2	0.9995	2
						TLFIQCDVADQQQLR	2	0.9997	3
						TLFIQCDVADQQQLR	3	0.9979	2
						VALVDWNLEAGVQCK	2	0.9997	2
						VALVTGAAQIGIR	2	0.9997	1
Q5701-1	P16152	CBR1_HUMAN	CBR1	Carbonyl reductase [NADPH] 1	1.0000	51.62	12	13	22
						DVCTELLPLKPGQR	2	0.9995	3
						DVCTELLPLKPGQR	3	0.9973	2
						EYGGDLVNNAGIAFK	2	0.9992	2
						FHQLDIDLOSIR	3	0.9993	2
						FRSETITEELVGLMKN	3	0.949	1
						GIGLAIVR	2	0.9939	1
						GQAAVOQLQAEGLSPR	2	0.9995	2
						IGVTVLSR	2	0.9933	1
						ILINACPGWVVR	2	0.9995	3
						LFSGDVLTAR	2	0.9908	1
						LGVTVLSR	2	0.9874	1
						TNFFGTR	2	0.9992	1
						VVNVSIMSVR	2	0.9983	2
Q5702-1	P16444	DPEP1_HUMAN	DPEP1	Dipeptidase 1	0.9478	4.87	1	1	1
						VPEGLDVSQYPLDIAELLR	3	0.9478	1
Q5703-1	P17858	PFKAL_HUMAN	PFKL	ATP-dependent 6-phosphofructokinase, liver type	1.0000	11.67	8	9	12
Q5703-2	P17858-2	PFKAL_HUMAN	PFKL	Isoform 2 of ATP-dependent 6-phosphofructokinase, liver type	1.0000	11	8	9	12
						GQLESIVENIR	2	0.9602	1
						IMEVIDAITTAQSHQR	3	0.8135	1
						LNIIIAEGAIDR	2	0.9801	2
						MGIVYGAK	2	0.8421	1
						SEWGSLEELVAEGK	2	0.9992	2
						SEWGSLEELVAEGK	3	0.9891	1
						TPVLEVNGR	2	0.9965	2
						VNVEHMTKE	2	0.9536	1
						VTVLGHVQR	2	0.9913	1
Q5704-1	P17900	SAP3_HUMAN	GM2A	Ganglioside GM2 activator	1.0000	13.99	2	2	3
						SEFVVPDLEPSWLTGNYR	2	0.9996	2
						VDLVLEK	2	0.9751	1
Q5705-1	P17987	TCPA_HUMAN	TCP1	T-complex protein 1 subunit alpha	1.0000	17.81	9	9	13
						EQLAIAEFAR	2	0.9985	2
						FATEAAILTLR	2	0.9996	2
						IACIDFSLQK	2	0.9871	1
						ICDDELIIK	2	0.9962	2
						LLEVEHPAK	2	0.9991	1
						SQNVMAASIANIVK	2	0.9914	1
						SSLGPVGLDK	2	0.9919	1
						TSASILR	2	0.9936	1

						YINENLVNTDELGR	2	0.9995	2
Q5706-1	P18085	ARF4_HUMAN	ARF4	ADP-ribosylation factor 4	1.0000	57.22	7	7	11
						DAVLLLFANK	2	0.9979	1
						ILMVGLDAAGK	2	0.9979	2
						IQEVADELQK	2	0.9944	1
						LGEVITPTITGNNVETVEYK	2	0.9984	2
						MULVVELR	2	0.9955	1
						NICTTVWDVGGQDR	2	0.9784	2
						TWVQATCATQGTGLYEGDLWLSNELSKR	3	0.999	2
Q5707-1	P18206-2	VINC_HUMAN	VCL	Isoform 1 of Vinculin	0.9715	1.78	1	1	1
Q5707-2	P18206-3	VINC_HUMAN	VCL	Isoform 3 of Vinculin	0.9715	8.56	1	1	1
Q5707-3	P18206	VINC_HUMAN	VCL	Vinculin	0.9715	1.68	1	1	1
Q5708-1	P19012	K1C15_HUMAN	KRT15	Keratin, type I cytoskeletal 15	1.0000	GILSGTSDLLLTDFEAEVR	2	0.9715	1
						5.04	1	1	1
						GGSLAGGGGFGGSLSGGGGSR	3	0.9291	1
Q5709-1	P19021-2	AMD_HUMAN	PAM	Isoform 2 of Peptidyl-glycine alpha-amidating monooxygenase	0.9984	2.66	2	2	2
Q5709-2	P19021-3	AMD_HUMAN	PAM	Isoform 3 of Peptidyl-glycine alpha-amidating monooxygenase	0.9984	2.54	2	2	2
Q5709-3	P19021-4	AMD_HUMAN	PAM	Isoform 4 of Peptidyl-glycine alpha-amidating monooxygenase	0.9984	2.59	2	2	2
Q5709-4	P19021-5	AMD_HUMAN	PAM	Isoform 5 of Peptidyl-glycine alpha-amidating monooxygenase	0.9984	2.36	2	2	2
Q5709-5	P19021-6	AMD_HUMAN	PAM	Isoform 6 of Peptidyl-glycine alpha-amidating monooxygenase	0.9984	2.41	2	2	2
Q5709-6	P19021	AMD_HUMAN	PAM	Peptidyl-glycine alpha-amidating monooxygenase	0.9984	2.36	2	2	2
						IPVDEEAFVDFKPR	3	0.9844	1
						NNLVIFHR	2	0.9	1
Q5710-1	P19224-3	UD16_HUMAN	UGT1A6	Isoform 3 of UDP-glucuronosyltransferase 1-6	1.0000	7.22	2	2	3
Q5710-2	P19224	UD16_HUMAN	UGT1A6	UDP-glucuronosyltransferase 1-6	1.0000	6.02	2	2	3
						GAGVTNNVLEMTSEDLENALK	2	0.9993	2
						SFLTAPQTEYR	2	0.9802	1
Q5711-1	P19338	NUCL_HUMAN	NCL	Nucleolin	1.0000	27.46	21	23	46
						ALELTGLK	2	0.9984	1
						EVFEDAAEIR	2	0.9996	2
						FGYVDFESAEDLEK	2	0.9997	2
						FGFYVDFESFEDAK	2	0.9997	2
						GIAYIEFK	2	0.9995	1
						GIAYIEFKTEADAETKFEK	3	0.9948	3
						GLSEDTTEETLKSFDGSR	2	0.9987	1
						GYAFIEFASFEDAK	2	0.9997	5
						GYAFIEFASFEDAKAELNSCNKR	3	0.9884	3
						KFGYVDFESAEDLEK	2	0.9997	3
						KFGYVDFESAEDLEK	3	0.9987	1
						KFGYVDFESAEDLEKALELTGLK	3	0.9916	2
						LELQGR	2	0.9983	1
						NDLAVVDVR	2	0.9994	1
						NLPYKVTQDELK	2	0.9969	2
						NLPYKVTQDELKEVFEDAAEIR	3	0.9976	3
						SISLYPTGK	2	0.9955	1
						SISLYTGEKGQNDQYR	2	0.9944	1
						SKGYAFIEFASFEDAK	2	0.9334	1
						TGISDVFAK	2	0.9981	2
						TLVLSNLSYSATEETLQEVFEK	2	0.9997	4
						TLVLSNLSYSATEETLQEVFEK	3	0.9997	3
						VFGNEIK	2	0.9534	1
Q5712-1	P19652	A1AG2_HUMAN	ORM2	Alpha-1-acid glycoprotein 2	1.0000	17.91	3	3	5
						EHVAHLFLR	3	0.96	1
						EQLGEFYALDCLCIPR	2	0.9941	2
						WFYIASAFR	2	0.9996	2
Q5713-1	P19823	ITH2_HUMAN	ITH2	Inter-alpha-trypsin inhibitor heavy chain H2	1.0000	19.13	15	17	35
Q5713-2	Q57985	Q57985_HUMAN	ITH2	Inter-alpha-trypsin inhibitor heavy chain H2	1.0000	19.36	15	17	35
						AEDHFSVDIFQNIIR	2	0.9992	2
						AGLELVNFGYVHFAPDNLDPIPK	3	0.9961	4
						AHVSFKPTVAQQR	2	0.8992	1
						AYLTINQLLAER	2	0.954	2
						ETAVDGELVLYDYK	2	0.9994	4
						FLHVPDT	2	0.8882	1
						FYNQVSTPLLR	2	0.9695	2
						HLEVDVWVIEPQGLR	2	0.9996	2
						HLEVDVWVIEPQGLR	3	0.9942	2
						IQPSGGTNINEALLR	2	0.9993	3
						KLWAYLTINQLLAER	3	0.9958	2
						SSALDMENFR	2	0.997	2
						TEVAVLPGAK	2	0.9993	2
						VOFELHPQYK	2	0.9974	2
						VVNNSPQPNVVF	2	0.8102	1
						VVNNSPQPNVVFVDQIPK	2	0.9996	2
						VVNNSPQPNVVFVDQIPK	3	0.9932	1
Q5714-1	P20160	CAP7_HUMAN	AZU1	Azurocidin	1.0000	36.25	8	9	17
						CQVAGWGSQR	2	0.9973	1
						GPOFFTR	2	0.9993	2
						GPOFFTRV	2	0.9806	2
						HFCGGALIHA	2	0.8749	1
						HFCGGALIHAR	2	0.9965	1
						HFCGGALIHAR	3	0.9963	1
						OPFLASINQGR	2	0.9986	4
						RGGINSGDGGTPLVCEGLANGVASFSLSPGCR	3	0.9987	3
						VALFRDWIDGVLNPNPGF	2	0.9507	2
Q5715-1	P20851	C4BPB_HUMAN	C4BPB	C4b-binding protein beta chain	1.0000	42.06	9	11	26
Q5715-2	P20851-2	C4BPB_HUMAN	C4BPB	Isoform 2 of C4b-binding protein beta chain	1.0000	42.23	9	11	26
						ALLAFQESK	2	0.9997	2
						ESGMTMEELK	2	0.9981	1
						ESGMTMEELKYSLEK	2	0.9969	2
						EVEGILGTIVYCK	2	0.9997	2
						LIQEAPKPECEK	2	0.9997	2
						LIQEAPKPECEKA	2	0.9833	2
						NLCEAMENFMQQLK	2	0.9997	3
						NLCEAMENFMQQLK	3	0.9993	3
						SQCLEDTWVAPPFPICK	2	0.9995	4
						SQCLEDTWVAPPFPICK	3	0.993	4
						YYLVGVQEQQCVDEGWSSALPVCK	3	0.8682	1
Q5716-1	P20908	COSA1_HUMAN	COL5A1	Collagen alpha-1(V) chain	0.9999	1.58	2	2	2
						GDPGPGAGLPKG	2	0.9685	1
						GNEGPPGPPGPPGSPGER	2	0.9957	1
Q5717-1	P21266	GSTM3_HUMAN	GSTM3	Glutathione S-transferase Mu 3	1.0000	18.22	3	3	5
						LLLEFTDTSYEK	2	0.9994	2
						LTVDFTLYDILDQNR	2	0.9992	1
						VDIENQVMDFR	2	0.9946	2
Q5718-1	P21281	VATB2_HUMAN	ATP6V1B2	V-type proton ATPase subunit 8, brain isoform	1.0000	11.94	4	5	9
						AVVGEEALTSOLLYLEFLQK	2	0.8793	1
						LALTAEFLAVQCFK	2	0.9911	2
						NFIAGGPYENR	2	0.9197	2
						TVFETLDIGWQLLR	2	0.9997	3
						TVFETLDIGWQLLR	3	0.9616	1
Q5719-1	P21796	VDAC1_HUMAN	VDAC1	Voltage-dependent anion-selective channel protein 1	1.0000	36.75	8	8	14
						GYGFLIK	2	0.994	1
						LTLSALIDGK	2	0.9668	1
						LTLSALLDGK	2	0.9881	2
						TDEFQLHTNVNDGTEFGGSIYQK	3	0.9966	2
						VTQSNFAGVYK	2	0.9314	1
						WNTDNTLTGTEITVEDQLAR	2	0.9997	3
						WTEYGLTFTEK	2	0.998	2
						YQIDPDACFSAK	2	0.9994	2
Q5720-1	P21810	PGS1_HUMAN	BGN	Biglycan	1.0000	13.66	5	5	8
						IQAELEDLR	2	0.9996	2
						LAIOFGNY	2	0.9171	1
						LGIGHNQIR	2	0.9995	1

						VGWDFCPMGFGVK	2	0.9996	2
						VPSEGLPDLK	2	0.9995	2
Q5721-1	P21964	COMT_HUMAN	COMT	Catechol O-methyltransferase	1.0000	41.33	8	12	37
Q5721-2	P21964-2	COMT_HUMAN	COMT	Isoform Soluble of Catechol O-methyltransferase	1.0000	50.68	8	12	37
						AIYKGGSEAGP	2	0.9926	2
						DRYLPDTLLLECGLLR	3	0.9938	3
						GSSCFECHYOSFLEYR	2	0.9997	2
						GSSCFECHYOSFLEYR	3	0.9984	2
						GTVLADNVICPGAPDLAHVR	3	0.9994	4
						NDAVIQEHQPSVLELGAYCGYSAVR	3	0.9981	3
						KGTVLLADNVICPGAPDLAHVR	3	0.9993	2
						KGTVLLADNVICPGAPDLAHVR	4	0.9249	1
						LITIEINPDCAITQR	2	0.9997	7
						LITIEINPDCAITQR	3	0.9994	3
						YLPDTLLLECGLLR	2	0.9997	5
						YLPDTLLLECGLLR	3	0.9995	3
Q5722-1	P22314	UBA1_HUMAN	UBA1	Ubiquitin-like modifier-activating enzyme 1	1.0000	18.05	12	13	22
						AAVATFLQSQVPEFTPK	2	0.9935	2
						DNPGVVTCLDEAR	2	0.9996	2
						GGVUSQVK	2	0.9707	1
						KLAYVAAGDLAPINAFIGGLAAQEVIMK	3	0.9298	2
						KPLLESGTLGTK	2	0.9982	1
						LAGTQPLEVLEAVQR	2	0.9991	3
						LQTSVLVSLGR	2	0.9989	2
						NEEDAELVALAQAVNAR	2	0.9963	1
						NEEDAELVALAQAVNAR	3	0.9978	1
						SLVASLAEPDFVYDFAK	2	0.9967	1
						VLGPYTFISICDTSNFSQYIR	2	0.9996	2
						YDQGVAVFGSDLQEK	2	0.9975	1
						YFLVGAGAGCELLK	2	0.9997	3
Q5723-1	P22626	ROA2_HUMAN	HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	1.0000	9.92	4	5	8
Q5723-2	P22626-2	ROA2_HUMAN	HNRNPA2B1	Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	1.0000	10.26	4	5	8
						IDTIEITDR	2	0.9991	1
						KLFIGLSFETTESLR	2	0.9992	1
						KLFIGLSFETTESLR	3	0.9971	1
						LFIGLSFETTESLR	2	0.9997	4
						NYEQWQWK	2	0.9654	1
Q5724-1	P22891-2	PROZ_HUMAN	PROZ	Isoform 2 of Vitamin K-dependent protein Z	1.0000	46.21	53	63	164
Q5724-2	P22891	PROZ_HUMAN	PROZ	Vitamin K-dependent protein Z	1.0000	48.75	53	63	164
						AGLPVCTPEKDFAEHLIPR	3	0.9512	2
						APDLQDLPWQ	2	0.8409	1
						APDLQDLPWQV	2	0.8962	1
						APDLQDLPWQVK	2	0.9997	14
						APDLQDLPWQVR	3	0.8262	1
						APDLQDLPWQVNL	2	0.9882	3
						CLPGQESYTCSCAQGYR	2	0.9874	1
						DFAEHLIPR	2	0.9997	3
						DFCGVIIR	2	0.9997	6
						DFCGVIIRE	2	0.9134	1
						DFCGVIIREN	2	0.8656	2
						DLQDLPWQVK	2	0.95	1
						DQCACGVLTSKR	2	0.8811	1
						ENFVLTAK	2	0.9997	4
						FAEHLIPR	3	0.9754	1
						FCGGVIIR	2	0.9478	1
						GLLSGWAR	2	0.9997	4
						GSWFLTGVLG	2	0.9723	1
						GSWFLTGVLGSPQV	2	0.9915	2
						GSWFLTGVLGSPQVGGQ	2	0.8255	1
						GSWFLTGVLGSPQVGGQA	2	0.9075	1
						GSWFLTGVLGSPQVGGQAH	2	0.9976	3
						GSWFLTGVLGSPQVGGQAHMVL	2	0.9747	3
						GSWFLTGVLGSPQVGGQAHMVLTK	2	0.9997	1
						GSWFLTGVLGSPQVGGQAHMVLTK	3	0.9997	12
						GYTCTSPGYEGSNCELAK	2	0.9899	1
						KLTNSEGKDFCGGVIIR	3	0.9228	1
						LGEDHKQCVPHDQACG	2	0.9665	1
						LGEDHKQCVPHDQACGVLTSK	3	0.9991	3
						LGEDHKQCVPHDQACGVLTSK	4	0.9906	1
						LGEDHKQCVPHDQACGVLTSKR	3	0.9994	4
						LGEDHKQCVPHDQACGVLTSKR	4	0.9564	2
						LPQGESYTCSCAQGYR	2	0.9967	2
						LPVCTPEKDFAEHLIPR	3	0.9571	3
						LQDLPWQVK	2	0.8792	1
						LTNSEGKDFCGGVIIR	2	0.9995	4
						LTNSEGKDFCGGVIIR	3	0.9995	6
						LTNSEGKDFCGGVIIRE	2	0.8778	1
						LTNSEGKDFCGGVIIRE	3	0.8527	1
						LTNSEGKDFCGGVIIREN	2	0.8768	1
						LTNSEGKDFCGGVIIREN	3	0.8477	1
						NSEKDFCGGVIIR	2	0.8803	1
						PDLQDLRWQVK	2	0.9865	2
						QCVPHDQACGVLTSK	2	0.824	1
						QCVPHDQACGVLTSK	2	0.9997	2
						QCVPHDQACGVLTSK	3	0.9762	1
						QCVPHDQACGVLTSKR	2	0.9997	3
						QCVPHDQACGVLTSKR	3	0.999	4
						RAPDLQDLPWQ	2	0.986	4
						RAPDLQDLPWQV	2	0.9926	2
						RAPDLQDLPWQVK	2	0.9997	4
						RAPDLQDLPWQVK	3	0.9997	5
						SEKDFCGGVIIR	2	0.9747	1
						SPGYEGSNCELAK	2	0.9967	1
						SSVAAMHWMDGSSVTR	2	0.9997	5
						SSVAAMHWMDGSSVTR	3	0.9997	5
						TCTSPGYEGSNCELAK	2	0.9786	2
						TCTSPGYEGSNCELAK	2	0.9954	2
						TGDCQHFCLPGQES	2	0.946	1
						TDGQHFCLPGQESYTCSCAQGYR	3	0.9997	8
						TSQDPLMIK	2	0.9997	4
						TSQDPLMIKI	2	0.8467	1
						YDADAGENDLSL	2	0.8814	1
Q5725-1	P23284	PPIB_HUMAN	PPIB	Peptidyl-prolyl cis-trans isomerase B	1.0000	9.72	2	2	2
						IEVEKFAIAKE	2	0.9991	1
						VLEGMVVR	2	0.9971	1
Q5726-1	P23526	SAHH_HUMAN	AHCY	Adenosylhomocysteinase	1.0000	5.32	2	2	3
						VADIGLJAWKR	2	0.999	1
						VAVVAGVDVGK	2	0.9974	2
Q5727-1	P23526-2	SAHH_HUMAN	AHCY	Isoform 2 of Adenosylhomocysteinase	1.0000	2.97	1	1	2
						VAVVAGVDVGK	2	0.9974	2
Q5728-1	P24158	PRTN3_HUMAN	PRTN3	Myeloblastin	1.0000	27.73	6	8	20
Q5728-2	U3KPS2	U3KPS2_HUMAN	PRTN3	Myeloblastin	1.0000	33.02	6	8	20
						GNPGSHFCGGTLHPSFVLTAACHLR	3	0.9986	4
						GNPGSHFCGGTLHPSFVLTAACHLR	4	0.9944	2
						LVNVVLGAHNVR	2	0.9996	2
						LVNVVLGAHNVR	3	0.9853	1
						NVVLGAHNVR	2	0.8585	2
						TQPTQGHFSVAQVFLNNYDAENK	3	0.9996	4
						VALYVDWIR	2	0.9996	4
						VVLGAHNVR	2	0.8982	1
Q5729-1	P24534	EF1B_HUMAN	EEF1B2	Elongation factor 1-beta	1.0000	12.44	2	2	4
						SIQADGLVWSSK	2	0.9996	3
						SPAGLOVLNDYLADK	2	0.9987	1

Q5730-1	P25325	THTM_HUMAN	MPST	3-mercaptopyruvate sulfurtransferase	1.0000	13.47	3	4	9
Q5730-2	P25325-2	THTM_HUMAN	MPST	Isoform 2 of 3-mercaptopyruvate sulfurtransferase	1.0000	12.62	3	4	9
						AGQPLQLDASWYLPK	2	0.9996	4
						ALVSAQWVAEALR	2	0.9997	2
						ALVSAQWVAEALR	3	0.9857	1
						ARPDVSEGR	2	0.9995	2
Q5731-1	P25705	ATPA_HUMAN	ATPSA1	ATP synthase subunit alpha, mitochondrial	1.0000	12.55	12	14	25
						EAYPGDVFYLHSR	2	0.9903	1
						EIVTNFLAGFEA	2	0.9821	1
						EVAFAAQFGSLDAATOQLLSR	2	0.9997	3
						EVAFAAQFGSLDAATOQLLSR	3	0.998	2
						FENAFLSHVVSQHQAALLTIR	3	0.9618	1
						FENAFLSHVVSQHQAALLTIR	4	0.9442	1
						GMSLNLEPDNVGVVFGNDK	2	0.9994	2
						HALIYDDLK	2	0.997	1
						ILGADTSVLEETGR	2	0.9997	2
						NVQAEEVVEFSSGLK	2	0.9997	3
						TGAIVDPVGEELLGR	2	0.9996	3
						TGTAEMSSILEER	2	0.9995	2
						TSIAIDTIINGK	2	0.9946	2
						VLSGDGIAR	2	0.9989	1
Q5732-1	P25705-2	ATPA_HUMAN	ATPSA1	Isoform 2 of ATP synthase subunit alpha, mitochondrial	1.0000	8.75	3	3	6
						EAYPGDVFYLHSR	2	0.9903	1
						ILGADTSVLEETGR	2	0.9997	2
						TGAIVDPVGEELLGR	2	0.9996	3
Q5733-1	P25788-2	PSA3_HUMAN	PSMA3	Isoform 2 of Proteasome subunit alpha type-3	0.9931	4.84	1	1	2
Q5733-2	P25788	PSA3_HUMAN	PSMA3	Proteasome subunit alpha type-3	0.9931	4.71	1	1	2
						AVENSSTAIGIR	2	0.9931	2
Q5734-1	P25815	S100P_HUMAN	S100P	Protein S100-P	1.0000	86.32	5	7	12
						DKDAVDKLLK	2	0.9801	1
						DLDANGDAQVDFSEFIVVAITSACHK	3	0.9997	4
						ELPGFLOGSKDKDAVDK	2	0.9981	2
						MTELETAMGMIDVFSR	2	0.8558	1
						MTELETAMGMIDVFSR	3	0.9827	1
						YSGSEGSTQLTKGELK	2	0.9995	2
						YSGSEGSTQLTKGELK	3	0.912	1
Q5735-1	P26038	MOES_HUMAN	MSN	Moesin	1.0000	12.13	6	6	10
						APDFVYAPR	2	0.9896	1
						EVWFFGLQYQDTK	2	0.9981	3
						GMLREDAVLEYLK	3	0.9109	1
						IAQDLEMVGVNYFSIK	2	0.9845	1
						IGPPWSEIR	2	0.9994	2
						IKQVWHEHR	2	0.9991	2
Q5736-1	P26640	SYVC_HUMAN	VAR5	Valine-tRNA ligase	1.0000	10.52	10	10	13
						ADFPAGIPGECIDALR	2	0.8794	1
						CGEMAQASAAVTR	2	0.9919	2
						EAFLEQVWK	2	0.9472	1
						GALINVPPPLGLPR	2	0.9932	2
						IETMLGDVAVAVHPK	3	0.9738	1
						KAVLVALK	2	0.9942	1
						LHEEGIYR	2	0.993	1
						LSAAVTEAFVR	2	0.9994	1
						SLPIVDFEVDMDGTGAVK	2	0.9996	2
						VQGSQSDSEVVVATTR	2	0.9993	1
Q5737-1	P27169	PON1_HUMAN	PON1	Serum paraoxonase/arylesterase 1	1.0000	61.41	23	28	89
						AEGDFANGINISPDGK	2	0.9841	2
						DLNSEDPTVLELGITGSK	2	0.9567	1
						EVQPVLPNCNLVK	2	0.9997	4
						FDVSSFNPHGIST	2	0.9883	2
						FDVSSFNPHGISTFTDEDNAMYLLVNVHPPAK	3	0.999	5
						FDVSSFNPHGISTFTDEDNAMYLLVNVHPPAK	4	0.9925	1
						GDFANGINISPDGK	2	0.8638	1
						GIETGSEDLILPGLAFISSGLK	2	0.9997	5
						GIETGSEDLILPGLAFISSGLK	3	0.9996	3
						GIETGSEDLILPGLAFISSGLKYPGIGK	3	0.9993	9
						IFYDSENPPASEVLR	2	0.9997	9
						IFYDSENPPASEVLR	3	0.8542	1
						ILMLDLNEEDPTVLELGITGSK	2	0.9997	4
						ILMLDLNEEDPTVLELGITGSK	3	0.9994	3
						IONILTEPK	2	0.9997	3
						LLIGTVFHK	2	0.9992	2
						LLVNVHPPAK	2	0.8787	1
						NEEDPTVLELGITGSK	2	0.9006	1
						REVQPVLPNCNLVK	2	0.9564	1
						SFNPNSPGK	2	0.985	1
						STVELFK	2	0.994	1
						STVELFKFQEEK	2	0.9828	3
						TLGMLGLAFR	2	0.9894	2
						VTQVYAENGTVLQGSTVASVYK	2	0.9995	2
						VVAEGDFANGINISPDGK	2	0.9997	13
						YVYIAELLAH	2	0.9321	2
						YVYIAELLAHK	2	0.9996	3
						YVYIAELLAHK	3	0.9995	4
Q5738-1	P27348	1433T_HUMAN	YWHAQ	14-3-3 protein theta	1.0000	9.8	2	2	4
						AVTEQGAELSNEER	2	0.9994	3
						DSTLIMQLLR	2	0.997	1
Q5739-1	P27797	CALR_HUMAN	CALR	Calreticulin	1.0000	27.34	9	12	22
						EQFLDGDGWTSR	2	0.975	2
						FYALSASFEPFSNK	2	0.9997	3
						FYALSASFEPFSNK	3	0.998	2
						FYGDEEKDGLQTSQDAR	2	0.9996	1
						FYGDEEKDGLQTSQDAR	3	0.9933	1
						GQTLVVQGFVK	2	0.9997	3
						HEQNIQCGGGVVK	2	0.9997	2
						KVHVIFNYK	2	0.9916	2
						KVHVIFNYK	3	0.9337	1
						QIDNPDYK	2	0.9312	1
						SGTIFDNFLITNDEAYAEFGNETWGVTK	3	0.9995	3
						VHVIFNYK	2	0.9992	1
Q5740-1	P28066	PSA5_HUMAN	PSMA5	Proteasome subunit alpha type-5	0.9859	4.98	1	1	2
						LFQVEYAIEAIK	2	0.9859	2
Q5741-1	P28074-3	PSB5_HUMAN	PSMB5	Isoform 3 of Proteasome subunit beta type-5	0.9813	10	1	1	2
Q5741-2	P28074	PSB5_HUMAN	PSMB5	Proteasome subunit beta type-5	0.9813	6.08	1	1	2
						GYSYDLEVEQAYDLAR	2	0.9813	2
Q5742-1	P28799-3	GRN_HUMAN	GRN	Isoform 3 of Granulins	0.9998	8.23	1	1	2
						LQSGAWGCCPPTQAVCCEDHIHCCPAGFTCDTQK	4	0.9808	2
Q5743-1	P28799	GRN_HUMAN	GRN	Granulins	0.9998	8.43	2	2	3
Q5743-2	P28799-2	GRN_HUMAN	GRN	Isoform 2 of Granulins	0.9998	11.42	2	2	3
						LQSGAWGCCPPTQAVCCEDHIHCCPAGFTCDTQK	4	0.9808	2
						VHCCPHGAFCDLVHTR	4	0.8923	1
Q5744-1	P28838	AMPL_HUMAN	LAP3	Cytosol aminopeptidase	1.0000	9.63	4	4	6
Q5744-2	P28838-2	AMPL_HUMAN	LAP3	Isoform 2 of Cytosol aminopeptidase	1.0000	10.25	4	4	6
						ADMGGGAATCSAIVSAK	2	0.9107	1
						GITFDGGISIK	2	0.9813	2
						GVLFASGQNLAR	2	0.9994	2
						TUEFLLR	2	0.9882	1
Q5745-1	P29034	S10A2_HUMAN	S10A2	Protein S100-A2	0.9998	26.53	2	2	2
						ELPSFVGKVDDEGLK	2	0.967	1
						YSCGEGDKFK	2	0.9934	1
Q5746-1	P29350-3	PTN6_HUMAN	PTPN6	Isoform 2 of Tyrosine-protein phosphatase non-receptor type 6	0.9999	2.85	2	2	2
Q5746-2	P29350-4	PTN6_HUMAN	PTPN6	Isoform 4 of Tyrosine-protein phosphatase non-receptor type 6	0.9999	2.72	2	2	2
Q5746-3	P29350	PTN6_HUMAN	PTPN6	Tyrosine-protein phosphatase non-receptor type 6	0.9999	2.86	2	2	2
						LEVLSQSK	2	0.9537	1

						VGDQVTHIR	2	0.9916	1
Q5747-1	P29622	KAIN_HUMAN	SERPINA4	Kallistatin	1.0000	12.41	5	5	11
						FYYIASETPGK	2	0.9992	3
						IAPANADAFR	2	0.909	1
						IVDLVSELK	2	0.9774	2
						LGFTDLPSK	2	0.9978	3
						VGSALFSSHKL	2	0.9976	2
Q5748-1	P29692-3	EF1D_HUMAN	EEF1D	Isoform 3 of Elongation factor 1-delta	1.0000	21.4	5	4	11
						FYEQMGPIVAGASR	2	0.9997	2
						GVVQELQQAISK	2	0.9996	2
						GVVQELQQAISKLEAR	2	0.9948	1
						GVVQELQQAISKLEAR	3	0.9994	2
						IASLEVENQSLR	2	0.9997	2
						SIQLDGLVWGASK	2	0.9997	2
Q5749-1	P30041	PRDX6_HUMAN	PRDX6	Peroxiredoxin-6	1.0000	20.98	4	5	8
						DFTPVCTTELGR	2	0.9968	2
						FHDFLGDSWGILFSPR	3	0.9986	3
						FHDFLGDSWGILFSPR	4	0.9315	1
						LPPIPIIDDR	2	0.9349	1
						VVPVFGPOK	2	0.9796	1
Q5750-1	P30043	BLVRB_HUMAN	BLVRB	Flavin reductase (NADPH)	1.0000	18.45	3	4	6
						HDLGHFMLR	2	0.9178	1
						HDLGHFMLR	3	0.9986	1
						NDLSPTVMSEGAR	2	0.9991	1
						TVAGQDAVILLGTR	2	0.9996	3
Q5751-1	P30048-2	PRDX3_HUMAN	PRDX3	Isoform 2 of Thioredoxin-dependent peroxide reductase, mit	0.9369	5.88	1	1	2
Q5751-2	P30048	PRDX3_HUMAN	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	0.9369	5.47	1	1	2
						DYGVLLGSGLALR	2	0.9369	2
Q5752-1	P30084	ECHM_HUMAN	ECHS1	Enoyl-CoA hydratase, mitochondrial	0.9840	9.66	2	2	2
						AQFAQPEILIGTIPGAGGTQR	2	0.8255	1
						IVVAMAK	2	0.9884	1
Q5753-1	P30101	PDIA3_HUMAN	PDIA3	Protein disulfide-isomerase A3	1.0000	13.66	14	15	20
						EATNPPIVQEEKPK	2	0.9995	1
						ELSDISYLQR	2	0.9994	2
						FISDKDASIVGFFDDSPSEAHSEFLK	3	0.9975	2
						FLQDYFDGNLKR	3	0.9934	1
						FVMQEEFSR	2	0.9988	1
						IFRDGEEAGAYDGPR	3	0.9136	1
						KTFSHELSDFGLESTAGEIPVVAIR	3	0.9396	1
						LAPEYEAATR	2	0.9985	1
						LNFVAASR	2	0.9748	1
						LSKDPNIVIAK	2	0.9879	2
						LSKDPNIVIAK	3	0.9808	1
						RLAPEYEAATR	2	0.9578	1
						SDVALELTDONFESR	2	0.991	2
						SEPIPSNSDGPVK	2	0.9916	2
						TFSHELSDFGLESTAGEIPVVAIR	3	0.991	1
Q5754-1	P30153	2AAA_HUMAN	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory	1.0000	22.58	11	12	21
						ELVSDANQHVK	2	0.9947	1
						FSVCYPR	2	0.8942	1
						IGPILDNSTLQSEVKPILEK	3	0.9897	1
						LAGGDWFTSR	2	0.993	4
						LNIIISNLCVNEVIGIR	2	0.9995	2
						LNIIISNLCVNEVIGIR	3	0.8721	1
						LSTIALALGVER	2	0.9994	3
						LTQDQDVQVK	2	0.9989	3
						SEIPIPSNLASDQSGSVR	2	0.9786	1
						TSACGLFSVCYPR	2	0.9992	2
						VKEFCENLSADCR	2	0.9033	1
						VLELDNVK	2	0.9318	1
Q5755-1	P30447	1A23_HUMAN	HLA-A	HLA class I histocompatibility antigen, A-23 alpha chain	1.0000	24.93	7	7	12
						APWIEQEGPEYWEETGKVK	3	0.9961	3
						AYLEGTCDGLR	2	0.9973	1
						AYLEGTCDGLRR	2	0.8332	1
						CWALGFYPAEITLTWQR	2	0.9996	2
						FIAGVYDDTQFVR	2	0.9996	2
						SWTAADMAAQITQR	2	0.9693	1
						WAAVVPVSGEQR	2	0.9989	2
Q5756-1	P30520	PURA2_HUMAN	ADSS	Adenylosuccinate synthetase isozyme 2	0.9545	3.07	1	1	2
						VVDLLAQDADIVCR	2	0.9545	2
Q5757-1	P30740	ILEU_HUMAN	SERPINB1	Leukocyte elastase inhibitor	1.0000	38.52	12	14	29
						ADLSGMSGAR	2	0.9167	1
						FAYGYIEDLK	2	0.9984	3
						FKLEESYTLNSDLAR	2	0.996	2
						FQSLNADINKR	2	0.9988	3
						HNSSGSILFLGR	2	0.9871	3
						HNSSGSILFLGR	3	0.977	2
						KFAYGYIEDLK	3	0.9544	1
						KIEQLTLEK	2	0.99	1
						LGVDQLFNSSK	2	0.9954	2
						LVLYNAYFK	2	0.9991	1
						TFNFTVIEVNSR	2	0.9994	4
						TFNFTVIEVNSR	3	0.9598	1
						TYNFLPEFLVSTQK	2	0.9991	4
						VLELPYQGEELSMVILLPDDIEDSTGLK	3	0.8917	1
Q5758-1	P31431-2	SDC4_HUMAN	SDC4	Isoform 2 of Syndecan-4	1.0000	32.68	4	4	8
Q5758-2	P31431	SDC4_HUMAN	SDC4	Syndecan-4	1.0000	25.25	4	4	8
						AGSGSQVTEPK	2	0.9939	2
						ETEVIDPDLLGR	2	0.9997	3
						KLEENEVIPK	2	0.9868	1
						RISPVVEEDVSNK	2	0.9996	2
Q5759-1	P31939	PUR9_HUMAN	ATIC	Bifunctional purine biosynthesis protein PURH	1.0000	37.5	16	19	35
Q5759-2	P31939-2	PUR9_HUMAN	ATIC	Isoform 2 of Bifunctional purine biosynthesis protein PURH	1.0000	37.56	16	19	35
						AFHTAQGYDEASDYFR	3	0.9571	1
						DLVATIAVK	2	0.9994	2
						DYSELTGPEMLGGR	2	0.8681	1
						EVSDGIAPGYEEALTLSK	2	0.9994	6
						EVSDGIAPGYEEALTLSK	3	0.9968	2
						LDNFLIR	2	0.9996	2
						LTEVSISSDAFFPFR	2	0.9969	1
						LTEVSISSDAFFPFRDNVDR	3	0.9178	1
						MSSFQDFVALSDVCDVPTAK	2	0.9987	1
						NGQVIGIGAGQQR	2	0.9964	1
						TLFGLHLSQK	2	0.9671	1
						TLHPAVHAGILAR	2	0.9886	1
						TLHPAVHAGILAR	3	0.9203	1
						TVASPGVTVEEANKQIDIGVTLR	2	0.9996	1
						TVASPGVTVEEANKQIDIGVTLR	3	0.9996	6
						VCMVVDLYK	2	0.9951	2
						VVACNLVPEVK	2	0.9995	3
						VVIEACDELGIILAHNTLR	3	0.9442	1
						YTSQNSVCYAK	2	0.9759	1
Q5760-1	P31946	1433B_HUMAN	YWHAB	14-3-3 protein beta/alpha	1.0000	22.36	4	4	7
Q5760-2	P31946-2	1433B_HUMAN	YWHAB	Isoform Short of 14-3-3 protein beta/alpha	1.0000	22.54	4	4	7
						SVFYIYELNSPEK	2	0.9529	3
						TAFDEAIAEOLDTLNEESYK	2	0.9864	1
						YLIPNATQPEK	2	0.9948	1
						YLSEVASGDNK	2	0.9965	2
Q5761-1	P31947	1433S_HUMAN	SFN	14-3-3 protein sigma	1.0000	10.89	2	2	4
Q5761-2	P31947-2	1433S_HUMAN	SFN	Isoform 2 of 14-3-3 protein sigma	1.0000	12.5	2	2	4
						GAVEKEELSCEER	2	0.9987	2
						YLAEVATGDDKKR	2	0.9955	2
Q5762-1	P31949	S10AB_HUMAN	S100A11	Protein S100-A11	1.0000	25.71	2	2	6

						CESLAVRFQK	2	0.9996	3
						TETFSFAMNTELAFTK	2	0.9997	3
						12_32	3	0.9998	3
Q5763-1	P31997	CEAM8_HUMAN	CEACAM8	Carcinoembryonic antigen-related cell adhesion molecule 8	1.0000	EVLVVHVNLPQDPR	3	0.9517	1
						IIGVISNQITPGPAYSNR	3	0.9967	1
						TLTSLVTR	2	0.9942	1
Q5764-1	P32119	PRDX2_HUMAN	PRDX2	Peroxiredoxin-2	1.0000	27.78	7	7	11
						EGGLGPLNIPLADVTR	2	0.9993	2
						GLFIIDGK	2	0.9969	1
						KEGGLGPLNIPLADVTR	3	0.9981	2
						QITVNDLPVGR	2	0.9982	2
						RLSEYGVULK	2	0.9369	1
						RLSEYGVULKTDEGIAYR	3	0.9782	2
						TDEGIAYR	2	0.9902	1
Q5765-1	P33176	KINH_HUMAN	KIF5B	Kinesin-1 heavy chain	0.9981	2.63	3	3	3
						FRPINESVEVNR	2	0.9335	1
						NTIQWLELNLR	2	0.864	1
						TGAEGAVLDIAEK	2	0.9862	1
Q5766-1	P33908	MA1A1_HUMAN	MAN1A1	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	1.0000	27.41	17	21	44
						AAYLSGEEIFR	2	0.9765	3
						DILLEKK	2	0.9439	1
						DVYLHESYDVQSQSFLEATLK	3	0.9993	3
						FDGGVEAIATR	2	0.9997	6
						FVGGLLSAYLSGEEIFR	2	0.9997	5
						FVGGLLSAYLSGEEIFR	3	0.9994	4
						GATIVDALDTLFIMEMK	2	0.9996	2
						GHSSSLFGNIK	2	0.9984	1
						GHSSSLFGNIK	3	0.9824	1
						GLPPVDVFPPIGVESR	2	0.8729	1
						HAWNYYK	2	0.9602	1
						KMYFDAVQAIETHLIR	3	0.9996	2
						KMYFDAVQAIETHLIR	4	0.9431	1
						KSSSLTYIAEWK	2	0.9996	2
						KWAWEAVEALENHCR	3	0.985	1
						LGPFAFR	2	0.9927	1
						MYFDAVQAIETHLIR	3	0.9995	1
						SSSLTYIAEWK	2	0.9993	3
						WAWEAVEALENHCR	2	0.9925	2
						WAWEAVEALENHCR	3	0.9242	1
						YYLRPEVMEITYMYMWR	3	0.9983	2
Q5767-1	P34932	HSP74_HUMAN	HSPA4	Heat shock 70 kDa protein 4	1.0000	2.33	2	2	4
						AGGIETIANEYSOR	2	0.9664	2
						GCALQCILSPAFK	2	0.9991	2
Q5768-1	P35232	PHB_HUMAN	PHB	Prohibitin	0.9999	8.82	2	2	3
						FDAGELTQR	2	0.9931	1
						KLEAAEDIAYQLSR	3	0.9934	2
Q5769-1	P35442	TSP2_HUMAN	THBS2	Thrombospondin-2	1.0000	1.71	1	1	1
						DQGQGDACPDNDNDGVPDDR	3	0.9658	1
Q5770-1	P35527	KIC9_HUMAN	KRT9	Keratin, type I cytoskeletal 9	1.0000	83.47	37	48	112
						DIENQYETQITQIEHEVSSSGQEVSQSAK	3	0.9996	8
						DIENQYETQITQIEHEVSSSGQEVSQSAK	4	0.9817	2
						EIETHNLLEGQDEFSSGAGK	2	0.9997	3
						EIETHNLLEGQDEFSSGAGK	3	0.9996	4
						FSSSYSGGGSGR	2	0.9997	4
						GFSGASGGYSSSGFGGGFGGGSGGFGGFGGFGGAGGGDGILTANEK	4	0.9977	2
						GGGGGGGLSGGSGR	2	0.8788	1
						GGGGSGYSYSGGGSGGSGFASLLGGGFGGGSR	3	0.9995	4
						GGSGSGHGSGSGFGGSGSGSYGGGEASGGGYGGGSGK	3	0.9996	2
						GGSGSGHGSGSGFGGSGSGSYGGGEASGGGYGGGSGKS	3	0.9262	1
						GGSGSGYGGGSGGGGYGGSGSR	2	0.9997	4
						GGSGSGYGGGSGGGGSGGGYGGSGGGSGGSGGSHSGSGSGNYGGGSGSG	3	0.8009	1
						HGVQELIEIQSLSK	2	0.9997	3
						HGVQELIEIQSLSKK	2	0.9996	2
						HGVQELIEIQSLSKK	3	0.9997	3
						IKFEMEQNLR	2	0.9571	1
						IKFEMEQNLR	3	0.9963	1
						IQDWYDKK	2	0.993	1
						IQDWYDKKGPAAIQK	2	0.9885	1
						IQDWYDKKGPAAIQK	3	0.9893	1
						LASYLDKVALEAANNLENK	2	0.9996	3
						LASYLDKVALEAANNLENK	3	0.9992	3
						LEKEIETHYNLLEGQDEFSSGAGK	3	0.9994	3
						MRLEKEIETHYNLLEGQDEFSSGAGK	3	0.9171	1
						MTLDDFR	2	0.9993	2
						NHKEEMSQLTGQNSGDVNVEINVAPGK	3	0.9825	1
						NHKEEMSQLTGQNSGDVNVEINVAPGKDLTK	3	0.9942	1
						NHKEEMSQLTGQNSGDVNVEINVAPGKDLTK	4	0.9921	1
						NLLEGQDEFSSGAGK	2	0.9885	2
						NYSPPYNTIDILKQIDVLTGNNK	3	0.9995	4
						NYSPPYNTIDILKQIDVLTGNNK	4	0.8793	1
						NYSPPYNTIDILKQIDVLTGNNKTLDDINTR	3	0.9946	1
						QEIECQNEYSLLSIK	2	0.9996	4
						QEIECQNEYSLLSIK	3	0.9954	2
						QEYEQLIAK	2	0.9865	1
						QVLNLTMEK	2	0.9977	1
						QVLNLTMEKSDELMQYETLQEELMALK	3	0.9981	4
						QVLNLTMEKSDELMQYETLQEELMALKK	3	0.9759	2
						SDELMQYETLQEELMALK	2	0.9997	3
						SDELMQYETLQEELMALK	3	0.9889	2
						SDELMQYETLQEELMALKK	2	0.9993	2
						SDELMQYETLQEELMALKK	3	0.9944	3
						STMQELNSR	2	0.9996	6
						TLLDINTR	2	0.9995	2
						TLNDMRQEYEQIAK	2	0.9869	2
						VQALEAANNLENK	2	0.9997	2
						YCGQLQMIQEQISNLEAQITDVR	3	0.9996	3
						YCGQLQMIQEQISNLEAQITDVRQEIECQNEYSLLSIK	4	0.9524	1
Q5771-1	P35555	FBN1_HUMAN	FBN1	Fibrillin-1	0.9838	0.45	1	1	2
						YEDEECTPIAGR	2	0.9838	2
Q5772-1	P35579	MYH9_HUMAN	MYH9	Myosin-9	1.0000	46.89	93	117	233
						ADEWLMK	2	0.9937	1
						ADFCIHYAGK	2	0.9922	1
						ADFCIHYAGK	3	0.9175	1
						AGVLAHLEER	2	0.9993	1
						AKQTLENKELANEVK	2	0.9964	1
						ALEAMMDKALER	2	0.9842	1
						ALEDSNLYR	2	0.9997	2
						ALEQVQVEEMK	2	0.9995	1
						ALEQVQVEEMKTQLELEDLQATEDAK	3	0.9993	4
						ANLIQIQINTDLNLR	2	0.9997	2
						ANLIQIQINTDLNLR	3	0.9955	2
						ASITALEAK	2	0.9992	1
						ASREEILAQAK	2	0.9108	1
						ASREEILAQAK	3	0.8482	1
						ASREEILAQAKENEK	2	0.9972	1
						ASREEILAQAKENEK	3	0.9966	2
						DELADEIANSRGK	2	0.9995	1
						DFSALFSLQDQTQELLOEENR	2	0.9998	2
						DFSALFSLQDQTQELLOEENR	3	0.9997	2
						DFSALFSLQDQTQELLOEENRQK	3	0.9981	3
						DKADFCIHYAGK	3	0.8934	2
						DLEAHIDISANK	2	0.9997	2
						DLEGLSQR	2	0.9866	1

						DLEGLSORHEEK	2	0.9914	2
						EELAQAKENEK	2	0.9962	1
						ELEDATETADAMNR	2	0.9995	1
						ELESQISELOQDLESER	2	0.9997	4
						ELESQISELOQDLESER	3	0.9987	2
						EMEAELEDERK	2	0.9996	2
						EQLEEEFAHNLEK	2	0.9995	2
						FDQLAEFK	2	0.9825	1
						FVSELWK	2	0.9358	1
						GALALEEK	2	0.9927	1
						GALALEEKR	2	0.9992	1
						HSQAVEELAEQLEQTK	2	0.9991	1
						HSQAVEELAEQLEQTK	3	0.9853	2
						HSQAVEELAEQLEQTKR	3	0.9995	3
						IAEFTTNLTEEEK	2	0.9996	2
						IAEFTTNLTEEEKSK	2	0.9995	3
						IAQLEEELEEOGNTLINDR	2	0.9997	3
						IAQLEEELEEOGNTLINDR	3	0.9991	3
						IAQLEEELEEOGNTLINDRLK	3	0.9971	3
						IAQLEEQDNETK	2	0.9997	1
						IAQLEEQDNETKER	3	0.9228	1
						IIGLDQVAGMSETALPGAFK	2	0.9992	2
						IMGPIEEQMGLLR	2	0.9737	2
						IRELESQISELOQDLESER	2	0.9986	2
						IRELESQISELOQDLESER	3	0.9995	4
						ITDVIIFQACCR	2	0.9957	2
						KANLQIDQINTDLNLER	2	0.9996	1
						KANLQIDQINTDLNLER	3	0.9951	2
						KEEELQAALAR	2	0.9991	2
						KEEELQAALAR	3	0.996	1
						KEEELQAALARVEEEAAQK	3	0.8121	1
						KFDQLAEK	2	0.9778	1
						KKVEAQLEQLQVK	2	0.9991	2
						KKVEAQLEQLQVK	3	0.8102	1
						KLEEEQILEQDQCK	2	0.9997	3
						KLEEEQILEQDQCK	3	0.9768	1
						KLEGDSTDLSQIAELQAQIAELK	3	0.9996	8
						KMEDSVGCLATAEEVKR	3	0.9961	2
						KQLEEEICHDLEAR	3	0.9993	2
						KVEAQLEQLQVK	2	0.9997	2
						KVEAQLEQLQVK	3	0.9982	2
						KVIQYLVYVASSHK	3	0.9994	3
						LDPHVLVDQLR	2	0.9489	1
						LDPHVLVDQLR	3	0.9995	2
						LEGDSTDLSQIAELQAQIAELK	3	0.8805	1
						LEVNLOQAMK	2	0.9988	1
						LQLQEQQLAETLCAEAELR	3	0.9986	3
						LQQLFNDLVLVDHQR	2	0.9997	4
						LQQLFNDLVLVDHQR	3	0.9994	3
						LQQLFNHTMFILEQEYQYR	3	0.9995	3
						LQVELDNVTGLLSQSDSK	2	0.9997	6
						LQVELDNVTGLLSQSDSK	3	0.9991	2
						LRLEVNLOQAMK	3	0.9338	1
						LTEMETLOSQMAEK	2	0.9996	3
						LTKDPSALESQLODQELQEQENR	3	0.9942	4
						MEDSVGCLATAEEVKR	3	0.9218	1
						NFINNPLAQADWAAK	2	0.9996	2
						NKHEAMTDLEER	3	0.9936	1
						NLPYSEIENMYK	2	0.9989	2
						QAQERDELADEIANSNGK	2	0.9992	3
						QAQERDELADEIANSNGK	3	0.9965	1
						QIATLHAQVADMK	2	0.9994	2
						QIATLHAQVADMKK	2	0.9015	1
						QLEAEFEFAQR	2	0.9992	2
						QLLQANPILEAFGNK	2	0.9978	3
						QTLNERGELANEVK	2	0.9888	3
						RKLEGDSTDLSQIAELQAQIAELK	3	0.9957	2
						RKLEGDSTDLSQIAELQAQIAELK	4	0.9901	1
						SGFEPASLKEEYGEIAVELVENGKK	3	0.9769	2
						SMEAFEMQLQELAAER	2	0.9997	5
						TDLLEPYNK	2	0.9993	2
						TFHIFYLLSGAGEHLK	3	0.9996	3
						TFHIFYLLSGAGEHLK	4	0.998	4
						THEAQIQEMR	2	0.9996	2
						TLEFEAKTHEAQIQEMR	3	0.9873	1
						TQLEEELELQATEDAK	2	0.9997	3
						TRLQQLDLDLVLVDHQR	3	0.9993	4
						TVGQYKQLAK	2	0.9748	1
						VAAYDKLEK	2	0.988	1
						VEAQLEQLQVK	2	0.9995	1
						VEDMAELTCLNEASVLHNLIK	3	0.9921	2
						VIOYLVYVASSHK	2	0.9997	3
						VIOYLVYVASSHK	3	0.9996	2
						VISGVQLGNIVFK	2	0.9997	3
						VISGVQLGNIVFKK	2	0.9984	1
						VISGVQLGNIVFKK	3	0.9837	1
						VRTELADKVTK	2	0.9789	1
						VRTELADKVTK	3	0.9992	1
						VSHLLGINVTDFTFR	2	0.9996	3
						VSHLLGINVTDFTFR	3	0.9987	1
						VVFQEFR	2	0.9994	2
						YEILTPNSIPK	2	0.9978	2
						YKASITALEAK	2	0.9948	1
						YLVVDKNFINNPLAQADWAAK	3	0.9941	1
Q5773-1	P35579-2	MYH9_HUMAN	MYH9	Isoform 2 of Myosin-9	1.0000	2.03	3	3	5
						AGVLAAHEER	2	0.9993	1
						ALEDSNLYR	2	0.9997	2
						VVFQEFR	2	0.9994	2
Q5774-1	P35716	SOX11_HUMAN	SOX11	Transcription factor SOX-11	0.9321	4.08	1	1	1
						SAAGGGGSGAGGAGGAGK	2	0.915	1
Q5775-1	P35858	ALS_HUMAN	IGFALS	Insulin-like growth factor-binding protein complex acid labile	1.0000	8.6	3	3	3
Q5775-2	P35858-2	ALS_HUMAN	IGFALS	Isoform 2 of insulin-like growth factor-binding protein complex	1.0000	8.09	3	3	3
						LFQGLGKLEYLLSR	3	0.9015	1
						LWLEGNPWDCGCPK	2	0.9982	1
						SFEGLGQLEVLTDHNLQLEVK	3	0.8752	1
Q5776-1	P35908	K22E_HUMAN	KRT2	Keratin, type II cytoskeletal 2 epidermal	1.0000	46.17	26	28	57
						ADTEELACR	2	0.9986	1
						DVDNAYMIK	2	0.9739	2
						DYQELMNVK	2	0.9871	2
						FLEQONQVLQTK	2	0.9997	3
						GFSSGSVAVSSGSR	2	0.9993	2
						GGGFGGGSSFGGSGFGSGGFGGGGFGGGR	3	0.9351	1
						HGGGGGGFGGGGFGSR	2	0.9989	3
						HGGGGGGFGGGGFGSR	3	0.9984	2
						LALDVEIATYR	2	0.9976	1
						LEQQNQVLQTK	2	0.9924	1
						LNDEEALQQAQ	2	0.999	2
						LQGEIAHVYK	2	0.9954	2
						NKLNDEEALQQAQ	2	0.9901	3
						NKLNDEEALQQAQ	3	0.9929	2
						NKLNDEEALQQAQEDLAR	3	0.9979	3
						NLDLDSIAEVYK	2	0.9996	2
						NVQDAIADAEQR	2	0.9995	3

						SISVAGGGGGFGAAGGFGGR	2	0.9981	1
						SISVAGGGGGFGAAGGFGGR	2	0.9912	2
						SKEEAALYHSKYELQVTVGR	3	0.9989	2
						SVAGGGGGFGAAGGFGGR	2	0.9821	1
						TAAENDFVTLK	2	0.9158	1
						TAAENDFVTLK	2	0.9961	2
						VOLLNGIEFLK	2	0.9997	4
						VLYDAISQIHQSIVTDTNVLMSDNRSR	3	0.999	3
						WELLQAMNVGTRPINLEPIFGYDLSLR	4	0.9963	3
						YEELQVTVGR	2	0.9985	2
						YLDGLTAER	2	0.9949	1
Q5777-1	P36955	PEDF_HUMAN	SERPINF1	Pigment epithelium-derived factor	1.0000	29.67	11	13	24
						ALYYDLISPDHGTYS	2	0.9989	1
						ALYYDLISPDHGTYS	3	0.9759	1
						DTDTGALLFIGK	2	0.9996	3
						ELLDTVTAPQK	2	0.9482	1
						KTSLEDFYLDEER	2	0.9995	2
						KTSLEDFYLDEER	3	0.9981	2
						LAAAVSNFGYDLYR	2	0.9996	3
						LSYEDSPDFSK	2	0.9977	2
						LSYEGEYTK	2	0.9877	1
						SSFVAPLEX	2	0.9844	1
						TESIHR	2	0.9985	1
						TVQAVLTVPK	2	0.9978	2
						YGLSDLSCK	2	0.9984	4
Q5778-1	P39023	RL3_HUMAN	RPL3	60S ribosomal protein L3	0.9999	9.68	3	3	4
						AGMTHIVR	2	0.997	1
						NNASTDYDLSK	2	0.8779	1
						SINPLGGFVHYGEVNTDFV	2	0.978	2
Q5779-1	P39059	COFA1_HUMAN	COL15A1	Collagen alpha-1(XV) chain	1.0000	8.14	10	11	20
						DFAISVVKPSTR	2	0.9994	3
						DFAISVVKPSTR	3	0.9384	1
						FTGSLQQLTVHPD	2	0.9931	3
						FTGSLQQLTVHPDR	2	0.9974	3
						GGVLFATDAFQK	2	0.9995	3
						ILLYTEPGSHVS	2	0.9586	2
						ILLYTEPGSHVSQEAFAF	2	0.9065	1
						SSQALAFESSAGIFMGNAGATGLER	3	0.9568	1
						TLIPSTFFR	2	0.9979	1
						TLVNCCEHSR	2	0.9892	1
						VVYGLR	2	0.9952	1
Q5780-1	P39060	COIA1_HUMAN	COL18A1	Collagen alpha-1(XVIII) chain	1.0000	4.39	5	6	9
Q5780-2	P39060-1	COIA1_HUMAN	COL18A1	Isoform 2 of Collagen alpha-1(XVIII) chain	1.0000	5.07	5	6	9
Q5780-3	P39060-2	COIA1_HUMAN	COL18A1	Isoform 3 of Collagen alpha-1(XVIII) chain	1.0000	5.75	5	6	9
						ELLRETTGAALKPR	2	0.9785	2
						LTESYCEWIR	2	0.993	1
						QAMLGQVHEVPEGWLIPIFAEQEELYVR	3	0.9986	3
						TEAPSATGQASSLGGGR	2	0.9996	1
						YHFPSSLFR	2	0.9039	1
						YHFPSSLFR	3	0.9887	1
Q5781-1	P39656	OST48_HUMAN	DDOST	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	1.0000	3.95	2	2	3
Q5781-2	U3KQ84	U3KQ84_HUMAN	DDOST	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	1.0000	11.69	2	2	3
						GFELTFK	2	0.9969	1
						TLVLNDNLNVR	2	0.9994	2
Q5782-1	P40199	CEAM6_HUMAN	CEACAM6	Carcinoembryonic antigen-related cell adhesion molecule 6	1.0000	17.44	3	3	4
						EVLLLAHNLQNR	2	0.9993	2
						SDPTLVNLVIGSPDPTSPSK	2	0.9995	1
						VDGNSLVGVTVGTGQATPGPAYSGR	3	0.9522	1
Q5783-1	P40227	TCPZ_HUMAN	CCT6A	T-complex protein 1 subunit zeta	1.0000	33.52	11	11	18
						AQAALAVNISAAR	2	0.9994	2
						AQLGVQAFADALLIPK	2	0.9996	3
						GIDPFLDALSK	2	0.9945	1
						HKSETDTSIR	2	0.9768	1
						ITTEGFEAAKEK	2	0.9965	2
						KQDEPIDLFMIEIMEMK	3	0.9991	2
						QADLYISEGLHPR	3	0.9927	1
						QLLHSCVTIATNILLVDEIMR	3	0.9724	1
						VATAQDITGDGTTNSNVLIGELLK	3	0.9081	1
						VHAELADVLTEAVVDSILAIAK	3	0.9967	1
						VLAQNSGFDLQETLVK	2	0.9997	3
Q5784-1	P40227-2	TCPZ_HUMAN	CCT6A	Isoform 2 of T-complex protein 1 subunit zeta	1.0000	26.54	8	8	15
						AQAALAVNISAAR	2	0.9994	2
						AQLGVQAFADALLIPK	2	0.9996	3
						GIDPFLDALSK	2	0.9945	1
						ITTEGFEAAKEK	2	0.9965	2
						KQDEPIDLFMIEIMEMK	3	0.9991	2
						QLLHSCVTIATNILLVDEIMR	3	0.9724	1
						VHAELADVLTEAVVDSILAIAK	3	0.9967	1
						VLAQNSGFDLQETLVK	2	0.9997	3
Q5785-1	P40939	ECHA_HUMAN	HADHA	Trifunctional enzyme subunit alpha, mitochondrial	0.9402	1.97	1	1	1
						ADMVIAVFEDLSLK	2	0.9402	1
Q5786-1	P41218	MNDA_HUMAN	MNDA	Myeloid cell nuclear differentiation antigen	0.9999	5.65	2	2	4
						SLLAYDLGLTTK	2	0.9988	2
						VITISDYSECK	2	0.9636	2
Q5787-1	P41226	UBA7_HUMAN	UBA7	Ubiquitin-like modifier-activating enzyme 7	0.9598	1.48	1	1	1
						VLVSGQLGLAEVAK	2	0.9598	1
Q5788-1	P41252	SYIC_HUMAN	IARS	Isoleucine--tRNA ligase, cytoplasmic	1.0000	2.77	3	3	4
						GSELEITLIR	2	0.9818	1
						ILEFWTEFCFOELK	2	0.9978	2
						YIIIEELNVR	2	0.9564	1
Q5789-1	P42224	STAT1_HUMAN	STAT1	Signal transducer and activator of transcription 1-alpha/beta	1.0000	4.8	3	3	4
						EGAITFTWVER	2	0.9973	1
						NLSFLLTPPCAR	2	0.9208	1
						TELVSVSEVHPSR	2	0.9995	2
Q5790-1	P42330	AK1C3_HUMAN	AKR1C3	Aldo-keto reductase family 1 member C3	1.0000	33.13	8	10	22
Q5790-2	S4R322	S4R322_HUMAN	AKR1C3	Aldo-keto reductase family 1 member C3	1.0000	35.67	8	10	22
						HIDSAHLNNEEQVGLAIR	2	0.9997	3
						HIDSAHLNNEEQVGLAIR	3	0.9996	5
						HIDSAHLNNEEQVGLAIR	4	0.9975	1
						LAIEAGFR	2	0.9995	2
						NLHYFNSDSFASHPNPYPSEY	3	0.829	1
						QNVQVFEFQLTAEDMK	2	0.9996	3
						SKDVLVLAISALGSQR	3	0.9801	2
						TPALIALR	2	0.9995	2
						TPALIALRY	2	0.9522	1
						VIFDIVDLCTWEAMEK	2	0.9996	2
Q5791-1	P43490	NAMPT_HUMAN	NAMPT	Nicotinamide phosphoribosyltransferase	1.0000	10.79	4	4	7
Q5791-2	Q5SYT8	Q5SYT8_HUMAN	NAMPTL	Protein NAMPTL (Fragment)	1.0000	11.73	4	4	7
						NAQLNIELEAAHH	2	0.9995	2
						STQAPLIIRPDSGNPLDTVLK	3	0.9422	2
						SYSFDEIRK	2	0.9969	2
						YDGLHPIEK	3	0.9116	1
Q5792-1	Q13185	CBX3_HUMAN	CBX3	Chromobox protein homolog 3	0.9759	6.56	1	1	3
Q5792-2	P45973	CBX5_HUMAN	CBX5	Chromobox protein homolog 5	0.9759	6.28	1	1	3
						CPQIVAFYEER	2	0.9759	3
Q5793-1	P45974-2	UBP5_HUMAN	USP5	Isoform Short of Ubiquitin carboxyl-terminal hydrolase 5	0.9384	3.11	1	1	1
Q5793-2	P45974	UBP5_HUMAN	USP5	Ubiquitin carboxyl-terminal hydrolase 5	0.9384	3.03	1	1	1
						IGEWELIQESGVPLKPLFGPGYTGR	3	0.9384	1
Q5794-1	P46060	RAGP1_HUMAN	RANGAP1	Ran GTPase-activating protein 1	1.0000	8.69	4	4	4
						NRLNDSGATALAEAFR	3	0.8539	1
						QVEVINFGDCLVR	2	0.9871	1
						SSACFTLOELK	2	0.9947	1
						TQVAGGQLSEK	2	0.9013	1

Q5795-1	P46734	MP2K3_HUMAN	MAP2K3	Dual specificity mitogen-activated protein kinase kinase 3	0.9996	8.93	2	2	2
Q5795-2	P46734-2	MP2K3_HUMAN	MAP2K3	Isoform 1 of Dual specificity mitogen-activated protein kinase	0.9996	9.75	2	2	2
Q5795-3	P46734-3	MP2K3_HUMAN	MAP2K3	Isoform 2 of Dual specificity mitogen-activated protein kinase	0.9996	8.81	2	2	2
						FSPEFVDVDTAQLCR	2	0.9872	1
						NFEVEADDLVITSELGR	2	0.9661	1
Q5796-1	P46777	RL5_HUMAN	RPL5	60S ribosomal protein L5	0.9912	3.37	1	1	2
Q5796-2	Q577N0	Q577N0_HUMAN	RPL5	60S ribosomal protein L5 (Fragment)	0.9912	7.69	1	1	2
						DIICQIAYAR	2	0.9912	2
Q5797-1	P46940	IQGA1_HUMAN	IQGAP1	Ras GTPase-activating-like protein IQGAP1	1.0000	17.86	20	22	34
						ALESQDVNTVWK	2	0.9991	2
						ALQSPALGLR	2	0.999	2
						ATFYGEQVDYYK	2	0.9219	1
						EEIQSSISGVTAAYNR	2	0.9997	2
						EQLWLANEGLTR	2	0.9995	3
						FALGIFAINAVESGDVGK	2	0.9997	3
						FALGIFAINAVESGDVGK	3	0.9635	1
						FQPGETLLEITPATSEQAEHQ	3	0.9748	1
						GLQQQNSDWYK	2	0.9966	1
						GVLLIEDLQVWQFK	2	0.9993	1
						IGGILANELSVDEALHAIVIAINEADR	3	0.9903	1
						IGGNLLYR	2	0.8261	1
						ILAIGLINEALDEGDAQK	2	0.9988	1
						ILAIGLINEALDEGDAQK	3	0.9994	3
						LAVALINAAIQK	2	0.9993	1
						LEGVLAEAQHYQDTLIR	3	0.9975	2
						LGNFFSPK	2	0.9715	1
						NVIFEISPTTEVGDFEVK	2	0.9989	2
						RLAAVALINAAIQK	3	0.9993	2
						RLIVDVIR	2	0.996	1
						SNQQLENDLNLMDIK	2	0.9996	1
						TVLELMNPACQLPQVYFFAADLYQK	3	0.8559	1
Q5798-1	P48147	PPCE_HUMAN	PREP	Prolyl endopeptidase	1.0000	3.38	2	2	3
						SASGSDVWTK	2	0.971	1
						VLVYQDSLEGEAR	2	0.9994	2
Q5799-1	P48506	GSH1_HUMAN	GCLC	Glutamate--cysteine ligase catalytic subunit	0.9579	1.41	1	1	1
						GYVSDIDCR	2	0.9579	1
Q5800-1	P48507	GSH0_HUMAN	GCLM	Glutamate--cysteine ligase regulatory subunit	0.9789	4.74	1	1	2
						LFIVESNSSSTR	2	0.9789	2
Q5801-1	P48668	K2C6C_HUMAN	KRT6C	Keratin, type II cytoskeletal 6C	1.0000	40.96	21	22	40
						ADTLTDEINFLR	2	0.9995	3
						AIGGGLSVGGGSSTIK	2	0.9995	2
						ALYDAELSQMQTHISDTSVVLMDNNR	3	0.9992	3
						AQYEIIAQR	2	0.9986	1
						DVDAAAYMMNVLEQAK	2	0.9988	2
						EYQELMNVK	2	0.9948	1
						FLEQGNVLDTK	2	0.9015	1
						GGGLGGACGAGGFSR	2	0.9984	2
						ISIGGGSCAISGGYGR	2	0.9994	2
						LLKEYQELMNVK	2	0.9981	3
						NKLEGLDALQK	2	0.9622	1
						NMQDLVEDLK	2	0.9049	2
						QNLEPLFEQYNNLR	2	0.9977	3
						RQLDSVIGER	2	0.9846	1
						SRAEASWYQTK	2	0.9945	2
						SRAEASWYQTKYEELQVTAGR	3	0.9983	2
						SRGSGGLGACGAGGFSR	2	0.9981	2
						SRGSGGLGACGAGGFSR	3	0.8482	2
						TAAENFVTLK	2	0.9811	1
						TAAENFVTLK	2	0.9973	1
						WTLLEQGTQK	2	0.9985	1
						YEELQVTAGR	2	0.9991	2
Q5802-1	P48741	H5P77_HUMAN	HSPA7	Putative heat shock 70 kDa protein 7	1.0000	14.17	4	4	7
						ARFEELCSOLF	2	0.9883	1
						ATAGDTHLGGEDFNR	2	0.9976	1
						TPSPVAFDTER	2	0.9997	3
						VEIANDQGNR	2	0.9988	2
Q5803-1	P49257	LMAN1_HUMAN	LMAN1	Protein ERGIC-53	0.9052	2.35	1	1	1
						YVSSLTEISKR	2	0.9052	1
Q5804-1	P49327	FAS_HUMAN	FASN	Fatty acid synthase	1.0000	32.5	58	62	112
						ALQGEELQCLK	2	0.9994	3
						ACLDTAVERNPSLK	2	0.9986	1
						ALGLGVQLPVVFEDVVLHQATLPK	3	0.994	1
						CVILSNLSSTSHVPEVDGSAELQK	3	0.9972	2
						DLVEAAVHLGIR	2	0.9997	1
						DNLEFFLAGIR	2	0.9958	2
						DPSQQLPR	2	0.9992	1
						DTVITISGQAPVFEFVQLRK	3	0.8791	1
						EACPELDYFVSVSSVSGR	2	0.9997	8
						EAHLPPGAMAAGLSWEECK	3	0.9243	1
						EDGLAQQTQLNLR	2	0.9979	1
						EGGFLLLHTLRL	3	0.8969	1
						ELNVLVSVR	2	0.9979	2
						EYVWALVQAGIR	2	0.9931	1
						FDASFFGVHPK	3	0.9983	1
						GLVQALQTK	2	0.9997	1
						GVDLVLNSLAEK	2	0.9996	2
						GYAVLGGGR	2	0.9749	1
						GYDYGPHFGQILEASLEGDSGR	3	0.9995	4
						HAQPTCPGAQLCTVYVYSLNFR	3	0.9977	3
						HFLLEEDKPEPTAHAFVSTLIR	4	0.9926	1
						HGLVLPTR	2	0.9923	1
						IPGLSPHPLL	2	0.8947	2
						IPGLSPHPLLQ	2	0.9972	3
						LFDHPESPTPNPFERPLAQAEVYK	3	0.9992	5
						LGMLSPGTCCK	2	0.9774	1
						LLEQGLR	2	0.9563	1
						LLLEVTYEAIVDGGINPDSLR	3	0.9996	1
						LNSVQSSERPLFLVHPIEGSTTVFHSLSAR	4	0.9945	2
						LPEDPLSLGLDSPALK	2	0.9997	4
						LQVVDQPLPVR	2	0.9996	2
						LSFFDFR	2	0.9997	5
						LSIPTYGLQCTR	2	0.9555	1
						MASCLEVLDFLNPQHMVLSFVLAEK	3	0.9933	1
						QEPFLIGSTK	2	0.967	1
						QVOPEGPYR	2	0.9983	1
						RQIQEQVPILEK	2	0.9969	3
						SDIAVNVFPELK	2	0.9971	1
						SEGVYAVLLTK	2	0.9991	2
						SEGVYAVLLTK	2	0.9994	1
						SLVNPPEGPTLMR	2	0.9989	1
						SLYQSAGVAPSEFYIEAHGTGK	2	0.9948	1
						SLYQSAGVAPSEFYIEAHGTGK	3	0.9798	1
						TGGAYGEDLGADYNLSQVCDGK	2	0.9997	2
						TGTVSLEVR	2	0.9956	1
						TLEGGSLGSIHSSSLAEPR	2	0.9996	1
						TLEGGSLGSIHSSSLAEPR	3	0.9996	3
						VAAAVDLIK	2	0.9996	3
						VFTTVGSAEKR	2	0.9987	2
						VGDPEQLNGTR	2	0.9979	1
						VLEALLPK	2	0.9995	1
						VLEALLPKGLEER	2	0.9972	1
						VLEALLPKGLEER	3	0.9595	1
						VLFPATGYLSVWK	2	0.9995	2

						VLQGLVMNVYR	2	0.9993	1
						VSVHIEGDHR	2	0.9997	2
						VSVHIEGDHR	3	0.9994	2
						VTVAGGVHISGLHTESAPR	3	0.985	1
						VVEVLAGHGLYSR	2	0.9996	2
						VVVQVLAEEPAVLK	2	0.9995	3
						WTSQSLGQMFSGR	2	0.8435	1
						YSGTLNLR	2	0.9942	2
							2	2	4
Q5805-1	P49902	SNTC_HUMAN	NT5C2	Cytosolic purine 5'-nucleotidase	1.0000	4.99	2	2	4
Q5805-2	Q5IUJ4	Q5IUJ4_HUMAN	NT5C2	Cytosolic purine 5'-nucleotidase (Fragment)	1.0000	10.57	2	2	4
Q5805-3	P49902-2	SNTC_HUMAN	NT5C2	Isoform 2 of Cytosolic purine 5'-nucleotidase	1.0000	5.26	2	2	4
						GLVFDLYGNLLK	2	0.9997	3
						SPEYESLGFELTVR	2	0.9997	1
Q5806-1	P50990-2	TCPQ_HUMAN	CCT8	Isoform 2 of T-complex protein 1 subunit theta	0.9706	1.89	1	1	1
Q5806-2	P50990-3	TCPQ_HUMAN	CCT8	Isoform 3 of T-complex protein 1 subunit theta	0.9706	2.11	1	1	1
Q5806-3	P50990	TCPQ_HUMAN	CCT8	T-complex protein 1 subunit theta	0.9706	1.82	1	1	1
						FAEAFEAIPIR	2	0.9706	1
Q5807-1	P50995	ANX11_HUMAN	ANXA11	Annexin A11	0.9997	3.17	1	1	3
Q5807-2	P50995-2	ANX11_HUMAN	ANXA11	Isoform 2 of Annexin A11	0.9997	3.39	1	1	3
						GVGTDAELIELASR	2	0.9988	3
Q5808-1	P51654	GPC3_HUMAN	GPC3	Glypican-3	1.0000	8.28	3	3	5
Q5808-2	P51654-3	GPC3_HUMAN	GPC3	Isoform 3 of Glypican-3	1.0000	7.96	3	3	5
						EYILSLELVNGMYR	2	0.9741	1
						LNMEQLQASMEKL	2	0.9994	2
						WVPETVPVPSDLQVCLPK	2	0.9985	2
Q5809-1	P52790	HXX3_HUMAN	HK3	Hexokinase-3	0.9132	1.63	1	1	1
						AAQLCGAGVAAVEK	2	0.9132	1
Q5810-1	P52895	AK1C2_HUMAN	AKR1C2	Aldo-keto reductase family 1 member C2	1.0000	29.1	5	5	10
						LDNGHFMPLVGFGTYPAAEVK	3	0.9336	1
						NLQLDYVDLYLHFPVSVKPGEEVIPK	3	0.9978	2
						QNVQVHEFQLTSEEMK	2	0.9997	3
						SGVSNRNHR	2	0.9954	2
						YLTLDIFAGPPNYPFSDEY	2	0.9953	2
							1	1	1
Q5811-1	P53597	SUCA_HUMAN	SUCLG1	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitoch	0.9813	7.51	3	0.9127	1
						EKISALQAGVVSMSPAQLGTTIYK	3	0.9127	1
Q5812-1	P53621	COPA_HUMAN	COPA	Coatomer subunit alpha	1.0000	6.62	6	6	8
Q5812-2	P53621-2	COPA_HUMAN	COPA	Isoform 2 of Coatomer subunit alpha	1.0000	6.57	6	6	8
						ASNLENSTYDLYTIPIK	2	0.982	1
						CPLSGACYSPEFK	2	0.9995	2
						GFFEGTIASK	2	0.9979	1
						GITGVDLFGTTDAVVK	2	0.8849	1
						SSGLTAVVWAR	2	0.9083	1
						VTTVTEIGDVGILR	2	0.9992	2
Q5813-1	P53634	CATC_HUMAN	CTSC	Dipeptidyl peptidase 1	1.0000	23.54	9	9	22
						DPFNFELTNHVLVVGDTGDSAGMDYVWK	3	0.9996	2
						GTDECAIESIAVAATPIPK	2	0.9995	3
						GTDECAIESIAVAATPIPK	3	0.9866	1
						GTDECAIESIAVAATPIPKL	2	0.9997	4
						GTDECAIESIAVAATPIPKL	3	0.9954	2
						NSWGTGWGNGYFR	2	0.9995	3
						NVHGINFVSPVR	3	0.996	1
						NWACFTGK	2	0.9735	1
						RGTDCAIESIAVAATPIPK	3	0.9967	2
						RGTDCAIESIAVAATPIPKL	3	0.9987	2
						YYSSEHYHGGFYGGCNEALMK	3	0.998	1
Q5814-1	P53999	TCF4_HUMAN	SUB1	Activated RNA polymerase II transcriptional coactivator p15	1.0000	18.9	3	3	5
						EQSIDDAVR	2	0.9431	1
						GISLNPEQWSQLK	2	0.9992	2
						GISLNPEQWSQLKEQISDIDDAVR	3	0.9972	2
Q5815-1	P54136	SYRC_HUMAN	RARS	Arginine-tRNA ligase, cytoplasmic	1.0000	14.39	8	8	12
						IVFVPGCSPLTIYK	2	0.998	2
						LFEFAGYDVLIR	2	0.9996	3
						LLQEEEEK	2	0.9943	1
						LDNVIFSFK	2	0.9971	1
						SDGGYTYTSDLAIAIK	2	0.9326	1
						SLTAEIDRLK	2	0.9876	1
						STIHGESISR	2	0.9856	2
						VEIAGPGFINVHLR	3	0.9926	1
Q5816-1	P54868	HMCS2_HUMAN	HMGS2	Hydroxymethylglutaryl-CoA synthase, mitochondrial	1.0000	7.68	2	3	5
Q5816-2	P54868-2	HMCS2_HUMAN	HMGS2	Isoform 2 of Hydroxymethylglutaryl-CoA synthase, mitochond	1.0000	8.37	2	3	5
Q5816-3	P54868-3	HMCS2_HUMAN	HMGS2	Isoform 3 of Hydroxymethylglutaryl-CoA synthase, mitochond	1.0000	8.61	2	3	5
						IGAFSYGSLAASFSSFR	2	0.9995	3
						IGAFSYGSLAASFSSFR	3	0.9062	1
						VNFSPPGDTNSLFPGTWYLR	2	0.9988	1
Q5817-1	P55010	IF5_HUMAN	EIF5	Eukaryotic translation initiation factor 5	1.0000	2.32	2	2	4
						VNILDFVK	2	0.9973	2
						VNILDFVK	3	0.9976	2
Q5818-1	P55072	TERA_HUMAN	VCP	Transitional endoplasmic reticulum ATPase	1.0000	30.4	18	19	35
						AIANECQANFSIK	2	0.9993	2
						AIGVKPPR	2	0.9519	1
						DVQLEFLAK	2	0.9869	1
						ETVVEVPQVFWIDGGLGVK	3	0.9228	1
						EVQIGIPDATGR	2	0.9904	2
						GVLYFPQPGCK	2	0.9972	1
						IVSQLLTMDGLK	2	0.9921	1
						LADDVDLEQVANETHGHVGDALALCSEALQAIR	3	0.9177	1
						LAGESESNLR	2	0.9993	2
						LDQLIYPLPDEK	2	0.9988	2
						LEILQIHTK	3	0.9818	1
						LGDVISIQPCDVK	2	0.9993	2
						LIVDEAINEDSVVLSQPK	2	0.9996	3
						LIVDEAINEDSVVLSQPK	3	0.9964	2
						MDLQLFR	2	0.999	1
						NAPHIIRIDELDAIAPK	2	0.9996	5
						QAAPCVLFFDELDSIAK	2	0.9997	5
						VLFDFELDSIAK	2	0.8913	1
						WALSQSNPSALR	2	0.9997	1
Q5819-1	P55291	CAD15_HUMAN	CDH15	Cadherin-15	1.0000	2.7	1	2	4
						FSILQQSGPELPSIDELTGEIR	2	0.9997	2
						FSILQQSGPELPSIDELTGEIR	3	0.9993	2
Q5820-1	P55884	EIF3B_HUMAN	EIF3B	Eukaryotic translation initiation factor 3 subunit B	1.0000	2.83	2	2	4
Q5820-2	P55884-2	EIF3B_HUMAN	EIF3B	Isoform 2 of Eukaryotic translation initiation factor 3 subunit	1.0000	2.63	2	2	4
						GTQGVVTFEIR	2	0.999	2
						GTYLATFHQR	2	0.983	2
Q5821-1	P58107	EPIPL_HUMAN	EPK1	Epiplakin	1.0000	2.1	6	7	12
						GFFDPNTHENTLYQLLER	3	0.9904	3
						GFFDPNTHENTLYVQLLR	3	0.99	1
						GSVAHQSELR	2	0.9186	1
						LLDAQLATGGLVCPARR	3	0.9288	1
						LSVEEAAVGVGGEIOEK	3	0.9908	1
						VTPGSGALQGSVSVWELLYR	2	0.9993	2
						VTPGSGALQGSVSVWELLYR	3	0.9995	3
Q5822-1	P59665	DEF1_HUMAN	DEFA1	Neutrophil defensin 1	1.0000	22.34	6	7	25
Q5822-2	P59666	DEF3_HUMAN	DEFA3	Neutrophil defensin 3	1.0000	22.34	6	7	25
						IPACIAGER	2	0.9996	6
						IPACIAGER	2	0.9994	5
						RIPACIAGER	2	0.9538	1
						RYGTCTVQGR	2	0.9889	3
						RYGTCTVQGR	3	0.9966	2
						YGTCTVQGR	2	0.9997	7
						YGTCTVQGR	2	0.9838	1
Q5823-1	RAGN08	RAGN08_HUMAN	ARPC4	Actin-related protein 2/3 complex subunit 4 (Fragment)	1.0000	10.39	1	1	3
Q5823-2	P5998-4	ARPC4_HUMAN	ARPC4	Isoform 4 of Actin-related protein 2/3 complex subunit 4	1.0000	10.26	1	1	3

						AENFFILR	2	0.9995	3
QS824-1	P60022	DEFB1_HUMAN	DEFB1	Beta-defensin 1	0.9985	33.82	1	1	2
						SDHYNCVSSGGQCLYSACPIFK	3	0.9927	2
QS825-1	P60174-4	TPIS_HUMAN	TP11	Isoform 4 of Triosephosphate isomerase	1.0000	40.12	5	5	14
						DCGATWVVLGHSE	2	0.9997	3
						HVFGESDELIGQK	2	0.9996	4
						IYGGSVTGATCK	2	0.9992	3
						SNVSDAVAQSTR	2	0.9997	1
						VVLAYEPVWAGTGK	2	0.9997	3
QS826-1	P60174-1	TPIS_HUMAN	TP11	Isoform 2 of Triosephosphate isomerase	1.0000	79.92	17	22	49
QS826-2	P60174	TPIS_HUMAN	TP11	Triosephosphate isomerase	1.0000	69.58	17	22	49
						DCGATWVVLGHSE	2	0.9997	3
						ELASQPDVDGFLVGGASKPEFVDINAK	3	0.9813	3
						ELASQPDVDGFLVGGASKPEFVDINAKQ	3	0.8996	2
						HVFGESDELIGQK	2	0.9996	4
						HVFGESDELIGQK	3	0.9967	1
						IJAAQNCYK	2	0.9997	1
						IYGGSVTGATCK	2	0.9992	3
						KQSLGELIGLNAAK	3	0.8281	1
						QSLGELIGLNAAK	2	0.9995	3
						RHVFGESDELIGQK	2	0.9959	1
						RHVFGESDELIGQK	3	0.9994	2
						SNVSDAVAQSTR	2	0.9997	1
						VAHALAELGLVIACIGEK	2	0.9997	3
						VAHALAELGLVIACIGEK	3	0.9992	3
						VAHALAELGLVIACIGEKLDER	3	0.9993	3
						VAHALAELGLVIACIGEKLDEREAGITEK	4	0.8514	1
						VIADNVKDWSK	2	0.9978	2
						VPADTEVVCAPPTAYIDFAR	2	0.9997	5
						VPADTEVVCAPPTAYIDFAR	3	0.9168	1
						VTNGAFTGISPMGIK	2	0.9994	1
						VVLAYEPVWAGTGK	2	0.9997	3
						VVLAYEPVWAGTGK	3	0.9995	2
QS827-1	P60709	ACTB_HUMAN	ACTB	Actin, cytoplasmic 1	1.0000	73.6	34	41	102
QS827-2	P63261	ACTG_HUMAN	ACTG1	Actin, cytoplasmic 2	1.0000	73.6	34	41	102
						AGFAGDDAPR	2	0.9997	5
						AIQAVLSYASGR	2	0.9488	2
						ALDFEQEMATAASSSSLEK	2	0.9851	2
						ALPHAILR	2	0.9389	1
						AVFPISVGRPR	2	0.9997	2
						AVLSYASGR	2	0.9869	2
						CPEALFQPSFLGMESCGIHETTFNSIMK	3	0.9996	5
						DESGPSIVHR	2	0.9707	2
						DGQVITIGNER	2	0.9355	1
						DLTDLMK	2	0.946	1
						DLYANTVLSGGTMYPGIADR	2	0.9997	3
						DSYVGDEAQSKR	2	0.9997	2
						EITALAPSTMK	2	0.9992	2
						EKLCYVALDFEQEMATAASSSSLEK	3	0.9572	2
						ETFTNPAMYVAIQAVLSYASGR	3	0.9813	3
						FRCPALFQPSFLGMESCGIHETTFNSIMK	3	0.9988	2
						GYSTTTAER	2	0.9996	4
						HQGVVMVGMGQK	2	0.9979	1
						IIAPPERK	2	0.9994	2
						IWHHTFY	2	0.8665	1
						IWHHTFYNELR	2	0.9994	3
						IWHHTFYNELR	3	0.9993	2
						KDLYANTVLSGGTT	2	0.9773	2
						KDLYANTVLSGGTMYPGIADR	2	0.9996	1
						KDLYANTVLSGGTMYPGIADR	3	0.9995	2
						LCYVALDFEQEMATAASSSSLEK	2	0.9997	3
						LCYVALDFEQEMATAASSSSLEK	3	0.9996	3
						LDLAGRDLTDYLMK	2	0.9936	3
						LSLYASGR	2	0.9821	2
						QAVLSYASGR	2	0.9604	1
						QEYDESGPSIVHR	2	0.9994	2
						QEYDESGPSIVHR	3	0.9827	1
						QEYDESGPSIVHRK	2	0.9878	1
						SYELPDGQVITIGNER	2	0.9998	13
						SYELPDGQVITIGNER	3	0.999	4
						TTGIVMDSGDGVTHTVPIYEGYALPHAILR	3	0.9995	3
						TTGIVMDSGDGVTHTVPIYEGYALPHAILR	4	0.9012	2
						VAIQAVLSYASGR	2	0.992	2
						VAPEEHVLLTEAPLNPK	2	0.9997	3
						VAPEEHVLLTEAPLNPK	3	0.9981	2
						YELPDGQVITIGNER	2	0.9535	2
QS828-1	P63000-2	RAC1_HUMAN	RAC1	Isoform B of Ras-related C3 botulinum toxin substrate 1	1.0000	13.74	3	3	6
QS828-2	P63000	RAC1_HUMAN	RAC1	Ras-related C3 botulinum toxin substrate 1	1.0000	15.1	3	3	6
QS828-3	P60763	RAC3_HUMAN	RAC3	Ras-related C3 botulinum toxin substrate 3	1.0000	15.1	3	3	6
						CVVVGDGAVGK	2	0.9993	4
						TVFDEAIR	2	0.8878	1
						YLECSALTQR	2	0.9867	1
QS829-1	P60953	CDC42_HUMAN	CDC42	Cell division control protein 42 homolog	1.0000	21.47	3	3	6
						CVVVGDGAVGK	2	0.9993	4
						NVFDEAILAALPEPEK	2	0.8882	1
						TPFLLVGTQIDLR	2	0.9987	1
QS830-1	Q5JYX0	Q5JYX0_HUMAN	CDC42	Cell division control protein 42 homolog (Fragment)	1.0000	17.65	2	2	5
QS830-2	P60953-1	CDC42_HUMAN	CDC42	Isoform 1 of Cell division control protein 42 homolog	1.0000	12.57	2	2	5
						CVVVGDGAVGK	2	0.9993	4
						TPFLLVGTQIDLR	2	0.9987	1
QS831-1	P61026	RAB10_HUMAN	RAB10	Ras-related protein Rab-10	1.0000	17	3	3	5
						AFLTLAEDILR	2	0.9994	2
						LLUGDSGVGK	2	0.985	2
						NIDEHANEEDVER	2	0.9994	1
QS832-1	P61158	ARP3_HUMAN	ACTR3	Actin-related protein 3	1.0000	10.77	4	4	6
						DITYFIQQLR	2	0.9994	2
						EFSDVGYSR	2	0.9812	1
						LPACVVDGCTGYTK	2	0.9988	2
						YSYVCPDLVK	2	0.9973	1
QS833-1	P61160	ARP2_HUMAN	ACTR2	Actin-related protein 2	1.0000	18.53	5	5	6
						CGYAGSNFPEHFIPALVGRPIIR	3	0.8743	1
						DLMVGDASELR	2	0.9955	2
						GYAFNHSADEFVTR	2	0.999	1
						HLWDYTFGPEK	2	0.9836	1
						LCYGYNIEQEQK	2	0.9829	1
QS834-1	P62834	RAP1A_HUMAN	RAP1A	Ras-related protein Rap-1A	1.0000	12.5	2	2	3
QS834-2	P61224-2	RAP1B_HUMAN	RAP1B	Isoform 2 of Ras-related protein Rap-1b	1.0000	16.79	2	2	3
QS834-3	P61224-1	RAP1B_HUMAN	RAP1B	Isoform 3 of Ras-related protein Rap-1b	1.0000	13.94	2	2	3
QS834-4	P61224-4	RAP1B_HUMAN	RAP1B	Isoform 4 of Ras-related protein Rap-1b	1.0000	16.2	2	2	3
QS834-5	P61224	RAP1B_HUMAN	RAP1B	Ras-related protein Rap-1b	1.0000	12.5	2	2	3
						INVNEIFYDLVR	2	0.9997	2
						LVLVLSGGVGK	2	0.9992	1
QS835-1	P61586	RHOA_HUMAN	RHOA	Transforming protein RhoA	1.0000	37.31	7	7	12
						EVFEMATR	2	0.8642	1
						HFCPNVPIVLGNKK	3	0.9995	2
						IGAFCYMECSAK	2	0.9988	2
						KLVIYVGDGACGK	2	0.9964	1
						LRPLSYPTDVLMLCF	2	0.8263	1
						LVIYVGDGACGK	2	0.984	2
						TCLINIFSK	2	0.9996	3
QS836-1	P61626	LYSC_HUMAN	LYZ	Lysozyme C	1.0000	52.03	8	8	13
						GISLANWMCIAK	2	0.9984	1
						LGMIDGYR	2	0.9993	1

						RLGMDGYR	2	0.9919	1
						SALLQDNADAVACAK	2	0.9892	2
						STDYGFQINSR	2	0.9996	4
						TPGAVNACHLCSALLQDNADAVACAK	3	0.9282	2
						VVRDPQGIR	2	0.9785	1
						WESGYNTR	2	0.9903	1
Q5837-1	P61970	NTF2_HUMAN	NUTF2	Nuclear transport factor 2	1.0000	74.8	2	0.9994	14
						ADEDPIMGFQHMFLLK	2	0.9994	1
						ADEDPIMGFQHMFLLK	3	0.9917	3
						IQHSTAQDHQPTPDSCISMVVGQLK	3	0.8574	1
						LALHNFG	2	0.9994	1
						LSSLPFQK	2	0.9981	1
						LSSLPFQKI	2	0.8813	1
						NINDAWVCTNDMFR	2	0.9997	3
						TQLGAVIDASCLTWEGQQFGK	3	0.587	3
Q5838-1	P61978	HNRPK_HUMAN	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	1.0000	8.86	3	4	5
Q5838-2	Q5T6W1	Q5T6W1_HUMAN	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	1.0000	13.4	3	4	5
Q5838-3	Q5T6W5	Q5T6W5_HUMAN	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	1.0000	9.58	3	4	5
Q5838-4	Q5T6W2	Q5T6W2_HUMAN	HNRNPK	Heterogeneous nuclear ribonucleoprotein K (Fragment)	1.0000	10.82	3	4	5
Q5838-5	P61978-2	HNRPK_HUMAN	HNRNPK	Isoform 2 of Heterogeneous nuclear ribonucleoprotein K	1.0000	8.84	3	4	5
Q5838-6	P61978-3	HNRPK_HUMAN	HNRNPK	Isoform 3 of Heterogeneous nuclear ribonucleoprotein K	1.0000	9.32	3	4	5
						GSDFDCELR	2	0.9962	1
						ILSISADIETGILKK	3	0.9021	1
						LUHOSLAGGIGVK	2	0.9917	1
						LUHOSLAGGIGVK	3	0.9986	2
Q5839-1	P61981	1433G_HUMAN	YWHAG	14-3-3 protein gamma	1.0000	19.03	4	4	6
						DSTLIMQLLR	2	0.997	1
						LGLALNYSVFYEQNAPEQACHLAK	3	0.988	2
						YLAEVATGEK	2	0.8873	1
						YLAEVATGEKR	2	0.9987	2
Q5840-1	P62081	RS7_HUMAN	RP57	40S ribosomal protein S7	0.9973	11.86	2	2	2
						AIIRFVPDLK	2	0.8956	1
						DVNFEPFQQL	2	0.9743	1
Q5841-1	P62140	PP1B_HUMAN	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	1.0000	11.93	4	4	6
						EIFLSQPILLEAPLK	2	0.9997	3
						FLNRHDLDIR	3	0.8421	1
						HDLDIR	2	0.937	1
						IVQMTAEVR	2	0.9977	1
Q5842-1	P62195	PR58_HUMAN	PSMC5	26S protease regulatory subunit 8	1.0000	17.98	5	5	7
Q5842-2	P62195-2	PR58_HUMAN	PSMC5	Isoform 2 of 26S protease regulatory subunit 8	1.0000	18.34	5	5	7
						GVCTEAGMYALR	2	0.9541	1
						IDILDSALLRPRG	3	0.963	1
						IEELQLLVNDK	2	0.9964	2
						LLREELQLLQEGSGSYGVEVVR	3	0.9983	2
						TMLELLNQLDGFATK	2	0.8268	1
Q5843-1	P62241	RS8_HUMAN	RP58	40S ribosomal protein S8	1.0000	23.56	4	5	9
						ELEFYLR	2	0.9757	1
						IIDVYVNASNNELVR	2	0.9997	2
						IIDVYVNASNNELVR	3	0.9908	2
						LDVGNFSWGSECTR	2	0.9995	2
						NCIVLIDTPYR	2	0.999	2
Q5844-1	P62258	1433E_HUMAN	YWHAE	14-3-3 protein epsilon	1.0000	19.61	4	4	6
Q5844-2	P62258-2	1433E_HUMAN	YWHAE	Isoform SV of 14-3-3 protein epsilon	1.0000	21.46	4	4	6
						HLIPAANTGESK	2	0.9831	1
						LICCDILDVLDK	2	0.9959	2
						SVFYIELNSPDR	2	0.9476	2
						VAGMDELTYEER	2	0.9994	1
Q5845-1	P62333	PR510_HUMAN	PSMC6	26S protease regulatory subunit 10B	1.0000	12.34	4	4	8
						ALQSVQGVGVLEK	2	0.9971	2
						HGEIDYEAIVK	2	0.9989	3
						HGEIDYEAIVKLSDFNGADLR	3	0.8186	1
						NVCTEAGMFAIR	2	0.9988	2
Q5846-1	P62424	RL7A_HUMAN	RPL7A	60S ribosomal protein L7a	0.9999	8.65	2	2	3
Q5846-2	Q5T8U2	Q5T8U2_HUMAN	RPL7A	60S ribosomal protein L7a	0.9999	15.23	2	2	3
						AGVNTVTTLVENK	2	0.999	2
						HWGNGVLGPK	2	0.9493	1
Q5847-1	P62701	RS4X_HUMAN	RP54X	40S ribosomal protein S4, X isoform	1.0000	20.91	5	5	9
						FDTGMLCMVTGGANLGR	2	0.9997	2
						LSNIFVIGK	2	0.999	1
						TRIVPPLRLK	3	0.9855	1
						VNDTIQIDLETGK	2	0.9991	2
						VNDTIQIDLETGKITDFIK	3	0.9958	3
Q5848-1	P62714	PP2AB_HUMAN	PPP2CB	Serine/threonine-protein phosphatase 2A catalytic subunit beta	1.0000	12.3	3	3	6
						ELDQWVQLNECK	2	0.9823	1
						NVVTIFSAPNYCYR	2	0.9996	2
						YSFLQFDPAPR	2	0.9996	3
Q5849-1	P62745	RHOB_HUMAN	RHOB	Rho-related GTP-binding protein RhoB	1.0000	4.59	1	1	3
Q5850-1	P62805	H4_HUMAN	HIST1H4A	Histone H4	1.0000	27.18	4	4	9
						DAVYTEHAH	2	0.9995	4
						ISGLIYEETR	2	0.9996	3
						ISGLIYEETR	2	0.9895	1
						VFLENVIR	2	0.9889	1
Q5851-1	P62820	RAB1A_HUMAN	RAB1A	Ras-related protein Rab-1A	1.0000	28.29	4	4	7
						EFADSLGIPFLTSAK	2	0.9674	2
						FADDTYTESYSTIGVDKF	2	0.9994	2
						LLUGDSGVGK	2	0.985	2
						MGPATAGGAEK	2	0.9107	1
Q5852-1	P62873	GBB1_HUMAN	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta	1.0000	18.82	4	4	5
						ELAGHTGYLSCCR	2	0.9973	1
						LLLAGYDDFCNVCNWDALK	2	0.9995	2
						LLVSASQDGK	2	0.9815	1
Q5853-1	P62873-2	GBB1_HUMAN	GNB1	Isoform 2 of Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta	1.0000	12.35	3	3	4
						ELAGHTGYLSCCR	2	0.9973	1
						LLLAGYDDFCNVCNWDALK	2	0.9995	2
						LLVSASQDGK	2	0.9815	1
Q5854-1	P62937	PPIA_HUMAN	PPIA	Peptidyl-prolyl cis-trans isomerase A	1.0000	74.55	10	13	33
						DIADVDEPLGR	2	0.9791	2
						EGMNIVEAMER	2	0.9942	1
						HTGFGILSMANAGPNTNGSQFFICTAK	3	0.9983	2
						IIPGFMCGGDFTFR	2	0.9992	5
						KITADCGQLE	2	0.9997	3
						SIYGEKFEDENFIK	2	0.9993	1
						TEWLDGKHVVFVK	2	0.9973	2
						TEWLDGKHVVFVK	3	0.9032	1
						VKEGMNIVEAMER	2	0.9979	1
						VKEGMNIVEAMER	3	0.8071	1
						VNPVTFFDIADVDEPLGR	2	0.9997	5
						VSSELFADKVPK	2	0.9991	5
						VSSELFADKVPK	3	0.9863	4
Q5855-1	P62995-3	TRA2B_HUMAN	TRA2B	Isoform 3 of Transformer-2 protein homolog beta	1.0000	15.96	2	2	3
Q5855-2	P62995	TRA2B_HUMAN	TRA2B	Transformer-2 protein homolog beta	1.0000	10.42	2	2	3
						GFAFVYFENVDDAK	2	0.999	1
						YGPADVSVIYDQQSR	2	0.9982	2
Q5856-1	P63151-2	2ABA_HUMAN	PPP2R2A	Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit	1.0000	7.88	3	3	7
Q5856-2	P63151	2ABA_HUMAN	PPP2R2A	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit	1.0000	8.05	3	3	7
						INLWHLEITDR	2	0.9972	2
						SFFSEIISDSVK	2	0.9994	2
						VVIFQIQGQENK	2	0.9989	3
Q5857-1	P63241	IFSA1_HUMAN	EIF5A	Eukaryotic translation initiation factor 5A-1	1.0000	34.42	3	3	6
Q5857-2	P63241-2	IFSA1_HUMAN	EIF5A	Isoform 2 of Eukaryotic translation initiation factor 5A-1	1.0000	28.8	3	3	6
						EDLRLEPGDLGKEIQK	3	0.8604	1

						VHLVGIDIFTGK	3	0.9992	2
						YDCGEEILTVLSAMTEAAVAIK	3	0.9996	3
Q5858-1	P63244	GBLP_HUMAN	GNB2L1	Guanine nucleotide-binding protein subunit beta-2-like 1	1.0000	46.37	10	10	15
						DETNYGIPQR	2	0.9825	1
						DVLSVAFSSONR	2	0.983	1
						FSPNSSNPIIVSCGWDK	2	0.9995	2
						GHNGWVYGIATTPQPMILSASR	3	0.9518	1
						HLTYLDGGDINALCFSPNR	3	0.9973	3
						IIVDELKQEVSTSSK	2	0.9995	2
						LWDLTTGTTTR	2	0.938	1
						VWQVTIGTR	2	0.9992	2
						YTVQDESHSEWVSCVR	3	0.9927	1
						YWLCATGPSIK	2	0.9997	1
Q5859-1	P67775-2	PP2AA_HUMAN	PPP2CA	Isoform 2 of Serine/threonine-protein phosphatase 2A catalytic subunit	1.0000	14.9	3	3	8
Q5859-2	P67775	PP2AA_HUMAN	PPP2CA	Serine/threonine-protein phosphatase 2A catalytic subunit	1.0000	12.3	3	3	8
						ELDQWIEQLNECK	2	0.9995	3
						NVVTIFSPNYCYR	2	0.9996	2
						YSFLQDFAPR	2	0.9996	3
Q5860-1	P68104	EF1A1_HUMAN	EEF1A1	Elongation factor 1-alpha 1	1.0000	26.19	12	15	29
Q5860-2	Q5VTE0	EF1A3_HUMAN	EEF1A3P5	Putative elongation factor 1-alpha-like 3	1.0000	26.19	12	15	29
						AAGVGFEAGISK	2	0.919	1
						EHALLAYTLGVK	2	0.9997	3
						EHALLAYTLGVK	3	0.9996	3
						EVSTYIK	2	0.9591	1
						EVSTYIKK	2	0.9833	1
						IGGIGTVPVGR	2	0.9997	2
						LPLQDVYK	2	0.9709	1
						QLVGVNKK	2	0.8689	1
						QTVAVGVK	2	0.9995	1
						STTTGHLIYK	2	0.9997	3
						VETGVLPKGMVVTFAPVNVVTEVK	3	0.9993	3
						YEEVKEVSTYIK	2	0.9988	3
						YEEVKEVSTYIK	3	0.9955	1
						YYVTIDAPGHR	2	0.9997	3
						YYVTIDAPGHR	3	0.9993	2
Q5861-1	P68363	TBA1B_HUMAN	TUBA1B	Tubulin alpha-1B chain	1.0000	12.42	6	6	19
						AVCMLSNTTAAIEAWAR	2	0.9996	5
						DVNAIAIATIK	2	0.999	2
						EIIDLVLDR	2	0.9997	4
						GHYTGKEIIDLVLDR	3	0.9994	2
						MLSNTTAAIEAWAR	2	0.9183	2
						SIQFVDWCPTGFK	2	0.9997	4
Q5862-1	P68366-2	TBA4A_HUMAN	TUBA4A	Isoform 2 of Tubulin alpha-4A chain	1.0000	23.56	10	11	28
Q5862-2	P68366	TBA4A_HUMAN	TUBA4A	Tubulin alpha-4A chain	1.0000	22.77	10	11	28
						AVCMLSNTTAAIEAWAR	2	0.9996	5
						AVCMLSNTTAAIEAWAR	3	0.9984	2
						AVFDLEPTVIDEIR	2	0.9993	3
						AYHEQLSVAEITNACFEPA	2	0.9601	2
						AYHEQLSVAEITNACFEPANQMVK	3	0.9994	3
						DVNAIAIAIK	2	0.9937	1
						MLSNTTAAIEAWAR	2	0.9183	2
						SIQFVDWCPTGFK	2	0.9997	4
						SIQFVDWCPTGFKV	2	0.9786	2
						SIQFVDWCPTGFKVGI	2	0.8202	1
						TIGGGDSDSTTFCTGAGK	2	0.9997	3
Q5863-1	P68371	TB84B_HUMAN	TUB84B	Tubulin beta-4B chain	1.0000	25.39	9	9	34
						ALTVPETQCMFADAK	2	0.9984	4
						AVLVDEPCTMDSVR	2	0.9997	7
						FWEVSDDEHGDPTGTYHGDSDLQLER	3	0.9997	8
						INVYNEATGGK	2	0.9997	4
						INVYNEATGGKY	2	0.9722	1
						INVYNEATGGKYVPR	2	0.9996	3
						LHFFMPGFAPLTSR	3	0.9695	2
						MSATFGNSTAIQELFK	2	0.8786	1
						YLTVAAVFR	2	0.9997	4
Q5864-1	P68871	HBB_HUMAN	HBB	Hemoglobin subunit beta	1.0000	95.92	112	153	475
						AFSDGLAHLNLK	2	0.9924	5
						AGVANALAHKYH	2	0.9134	1
						ALWGVNVDVGEALGR	2	0.9934	3
						ALWGVNVDVGEALGR	3	0.9401	2
						ATLSELHCDK	2	0.9013	1
						ATLSELHCDKLHVDPENFR	2	0.9749	3
						ATLSELHCDKLHVDPENFR	3	0.9066	1
						AVTALWGVNVDVGEALGR	3	0.8119	1
						DEVGGEALGR	2	0.9943	3
						DKLHVDPENFR	2	0.9673	3
						DKLHVDPENFR	3	0.9414	2
						EFTPPVQ	2	0.9852	2
						EFTPPVQAA	2	0.9036	1
						EFTPPVQAAAY	2	0.9937	2
						EFTPPVQAAAYQ	2	0.9971	2
						EFTPPVQAAAYQK	2	0.9997	8
						EFTPPVQAAAYQK	3	0.9774	1
						EFTPPVQAAAYQKV	2	0.9957	2
						EKSAVTALWKG	2	0.9214	1
						FATLSELHCDKLHVDPENFR	3	0.9151	1
						FFSFGDLSTPDVAMGNPK	2	0.9978	4
						FFSFGDLST	2	0.939	1
						FFSFGDLSTP	2	0.8555	1
						FFSFGDLSTPD	2	0.9975	5
						FFSFGDLSTPDA	2	0.9935	3
						FFSFGDLSTPDAV	2	0.9986	6
						FFSFGDLSTPDVAMGNPK	2	0.9998	19
						FFSFGDLSTPDVAMGNPK	3	0.9996	3
						FFSFGDLSTPDVAMGNPKV	2	0.9367	1
						FSDGLAHLNLK	2	0.9345	3
						FSDGLAHLNLK	3	0.8507	1
						GAFSDGLAHLNLK	2	0.9951	6
						GKVNVDVGEALGR	2	0.9861	3
						GKVNVDVGEALGR	3	0.9361	1
						GLAHLNLK	2	0.9422	1
						GNVLVCLVAHHFGK	2	0.9765	2
						GNVLVCLVAHHFGK	4	0.984	1
						GTATLSELH	2	0.9963	2
						GTATLSELHC	2	0.9972	2
						GTATLSELHCD	2	0.9956	3
						GTATLSELHCDK	2	0.9997	4
						GTATLSELHCDK	3	0.9498	1
						GTATLSELHCDKL	2	0.9511	2
						GTATLSELHCDKLHVD	2	0.9595	2
						GTATLSELHCDKLHVDPEN	2	0.924	1
						GTATLSELHCDKLHVDPENFR	2	0.9996	4
						GTATLSELHCDKLHVDPENFR	3	0.9995	8
						GTATLSELHCDKLHVDPENFR	4	0.9978	1
						HCDKLHVDPENFR	2	0.9801	2
						HCDKLHVDPENFR	3	0.8269	1
						HLPTEEK	2	0.9103	2
						HVDPENFR	2	0.9515	1
						KEFTPPVQAAAYQK	2	0.9652	1
						KLHVDPENFR	2	0.9703	1
						KLHVDPENFR	3	0.8815	1
						KSAVTALWKG	3	0.8747	1
						KVLGAFSD	2	0.8856	1

							KVLGAFSDGLAHL	2	0.961	2
							KVLGAFSDGLAHLN	2	0.9751	3
							KVLGAFSDGLAHLN	2	0.9889	2
							KVLGAFSDGLAHLN	2	0.9997	6
							KVLGAFSDGLAHLN	3	0.9997	12
							KVLGAFSDGLAHLN	4	0.9375	1
							KVNVDEVGGEALGR	2	0.9974	2
							KVNVDEVGGEALGR	3	0.9823	1
							LAHHFGK	2	0.9225	1
							LAHLN	2	0.8465	1
							LGNVLCVLAHHFGK	4	0.8854	1
							LHCDKLHVDPENFR	2	0.9735	2
							LHCDKLHVDPENFR	3	0.8133	1
							LHVDPENFR	2	0.9997	7
							LHVDPENFR	3	0.9996	4
							LLGNVLCV	2	0.9772	1
							LLGNVLCV	2	0.9694	2
							LLGNVLCV	2	0.9978	2
							LLGNVLCVLA	2	0.9959	2
							LLGNVLCVLAH	2	0.998	4
							LLGNVLCVLAHH	2	0.9971	2
							LLGNVLCVLAHH	3	0.987	2
							LLGNVLCVLAHHF	2	0.9974	5
							LLGNVLCVLAHHF	3	0.9875	2
							LLGNVLCVLAHHFG	2	0.9952	4
							LLGNVLCVLAHHFG	3	0.9826	1
							LLGNVLCVLAHHFGK	2	0.9997	5
							LLGNVLCVLAHHFGK	3	0.9997	6
							LLGNVLCVLAHHFGK	4	0.9995	9
							LLGNVLCVLAHHFGKE	2	0.9975	4
							LLGNVLCVLAHHFGKE	3	0.9892	3
							LLGNVLCVLAHHFGKE	4	0.9959	3
							LLGNVLCVLAHHFGKEFTPPVQ	3	0.8397	1
							LLVYYPW	2	0.9962	2
							LLVYYPWT	2	0.9952	3
							LLVYYPWTQ	2	0.9963	2
							LLVYYPWTQR	3	0.9994	5
							LSELHCDKLHVDPENFR	2	0.9902	3
							LSELHCDKLHVDPENFR	3	0.9641	1
							LVYYPWTQR	2	0.996	3
							LWGKVNDEVGGEALGR	3	0.9507	1
							NVDEVGGEALGR	2	0.871	1
							NVLCVLAHHFGK	2	0.9959	2
							NVLCVLAHHFGK	4	0.9885	2
							RLGNVLCVLAHHFGK	4	0.8258	1
							RLVYYPWTQR	2	0.9957	4
							RLVYYPWTQR	3	0.9801	2
							SAVTALWGK	2	0.9997	10
							SAVTALWGKV	2	0.835	1
							SAVTALWGKVNDEVGGEA	2	0.8945	2
							SAVTALWGKVNDEVGGEALGR	2	0.9996	6
							SAVTALWGKVNDEVGGEALGR	3	0.9996	14
							SAVTALWGKVNDEVGGEALGR	4	0.9949	1
							SDGLAHLN	2	0.9895	5
							SDGLAHLN	3	0.8253	1
							SELHCDKLHVDPENFR	2	0.9888	3
							SELHCDKLHVDPENFR	3	0.8897	1
							SELHCDKLHVDPENFR	4	0.9011	1
							TALWGKVNDEVGGEALGR	2	0.9919	2
							TALWGKVNDEVGGEALGR	3	0.956	1
							TLSELHCDK	2	0.977	1
							TLSELHCDKLHVDPENFR	2	0.9883	3
							TLSELHCDKLHVDPENFR	3	0.9697	2
							TPPVQAAYQK	2	0.9045	1
							VAGVANALAHK	2	0.9934	2
							VAGVANALAHKYH	2	0.9256	1
							VCVLAHHFGK	2	0.9923	3
							VDEVGGEALGR	2	0.9969	4
							VDPENFR	2	0.94	1
							VGEALGR	2	0.9882	2
							VHLTPEK	2	0.9997	11
							VLAHHFGK	2	0.9887	2
							VLGAFSDGLAH	2	0.8917	1
							VLGAFSDGLAHL	2	0.9865	6
							VLGAFSDGLAHL	2	0.992	4
							VLGAFSDGLAHLN	2	0.9941	4
							VLGAFSDGLAHLN	2	0.9966	8
							VLGAFSDGLAHLN	2	0.9998	18
							VLGAFSDGLAHLN	3	0.9997	13
							VLGAFSDGLAHLN	2	0.9329	2
							VLCVLAHHFGK	2	0.9919	2
							VNVDEVGGEALG	2	0.9976	3
							VNVDEVGGEALGR	2	0.9998	20
							VNVDEVGGEALGR	3	0.9996	4
							VNVDEVGGEALGR	2	0.9984	6
							VVAGVANALA	2	0.8581	1
							VVAGVANALAH	2	0.9932	2
							VVAGVANALAHK	2	0.9997	3
							VVAGVANALAHK	3	0.9993	1
							VVAGVANALAHKY	2	0.9757	2
							VVAGVANALAHKYH	2	0.9996	3
							VVAGVANALAHKYH	3	0.9919	1
							VVAGVANALAHKYH	4	0.9959	1
							VYYPWTQR	2	0.9788	2
							WGKVNDEVGGEALGR	2	0.9888	3
							WGKVNDEVGGEALGR	3	0.9445	1
Q5865-1	P69891	HBG1_HUMAN	HBG1	Hemoglobin subunit gamma-1	1.0000	23.81		3	3	5
Q5865-2	P69892	HBG2_HUMAN	HBG2	Hemoglobin subunit gamma-2	1.0000	23.81		3	3	5
							EFTPEVQASWQK	2	0.9978	2
							VLTLGDAIK	2	0.9761	1
							VNVEDAGGETLGR	2	0.9997	2
Q5866-1	P69905	HBA_HUMAN	HBA1	Hemoglobin subunit alpha	1.0000	85.92		62	87	202
							AAHLPAEFTPAVHASL	2	0.9975	2
							AAHLPAEFTPAVHASL	3	0.9926	4
							AAHLPAEFTPAVHASL	4	0.9913	2
							AFTTPAVHASL	2	0.9906	2
							AGEYGAELER	2	0.9932	2
							AHLPAEFTPAVHASL	2	0.996	3
							AHLPAEFTPAVHASL	3	0.9929	2
							AHLPAEFTPAVHASL	4	0.994	1
							AHVDDMPNALSALSDUHAHK	3	0.9528	1
							CLVTLAHLPAEFTPAVHASL	3	0.9735	4
							CLVTLAHLPAEFTPAVHASL	4	0.9854	2
							FLASVSTVLSK	2	0.9997	6
							FLASVSTVLSKY	2	0.9915	2
							GAHAGEYGAELER	2	0.9954	3
							GEYGAELER	2	0.9668	1
							GRVGAHAGEYGAELER	2	0.9893	2
							GRVGAHAGEYGAELER	3	0.8428	1
							HAGEYGAELER	2	0.9769	1
							HLPAEFTPAVHASL	2	0.9909	3
							HLPAEFTPAVHASL	3	0.993	1
							KVADALTNAVAHVDDMPNALSALSDUHAHK	3	0.9979	1

						KVADALNAVAHVDDMPNALSALSDLHAHK	4	0.9981	2
						KVGAHAGEYGAEALER	2	0.9875	1
						LLSHCLL	2	0.9592	1
						LLSHCLLV	2	0.9908	1
						LLSHCLLV	2	0.9293	1
						LLSHCLLVLT	2	0.9846	2
						LLSHCLLVTLA	2	0.8432	1
						LLSHCLLVTLAAH	3	0.8717	1
						LLSHCLLVTLAAHL	2	0.9765	3
						LLSHCLLVTLAAHL	3	0.8753	2
						LLSHCLLVTLAAHLP	2	0.9385	1
						LLSHCLLVTLAAHLP	3	0.9498	2
						LLSHCLLVTLAAHLP	2	0.9748	2
						LLSHCLLVTLAAHLP	3	0.9931	3
						LLSHCLLVTLAAHLP	3	0.9925	3
						LLSHCLLVTLAAHLP	2	0.8458	1
						LLSHCLLVTLAAHLP	2	0.9716	1
						LLSHCLLVTLAAHLP	2	0.9974	4
						LLSHCLLVTLAAHLP	3	0.9493	1
						LLSHCLLVTLAAHLP	2	0.984	2
						LLSHCLLVTLAAHLP	3	0.9893	2
						LLSHCLLVTLAAHLP	3	0.9907	6
						LLSHCLLVTLAAHLP	4	0.995	4
						LLSHCLLVTLAAHLP	3	0.9821	5
						LLSHCLLVTLAAHLP	4	0.9903	2
						LLSHCLLVTLAAHLP	3	0.9774	2
						LLSHCLLVTLAAHLP	3	0.9473	4
						LLSHCLLVTLAAHLP	3	0.8408	2
						LLSHCLLVTLAAHLP	4	0.889	1
						LLSHCLLVTLAAHLP	3	0.9991	5
						LLSHCLLVTLAAHLP	4	0.9996	6
						LLSHCLLVTLAAHLP	4	0.9168	1
						LP	2	0.9916	2
						LRVDPVNF	2	0.9995	2
						LRVDPVNF	3	0.9995	4
						LSALSDLHAHK	2	0.8625	1
						LVTAAHLP	3	0.8511	2
						MFLSPTTK	2	0.9997	4
						MFLSPTTK	2	0.985	2
						PAETTPAVHASL	2	0.9517	3
						PAETTPAVHASL	3	0.8465	1
						PAVHASL	2	0.9096	1
						PHFDLSHGAQV	3	0.9466	1
						TLAAHLP	2	0.966	1
						TLAAHLP	3	0.983	3
						TLAAHLP	4	0.9947	2
						TPAVHASL	2	0.8443	1
						TYPHFD	2	0.9842	1
						TYPHFDL	2	0.9933	5
						TYPHFDLSHG	2	0.9056	2
						TYPHFDLSHGAQ	2	0.9745	2
						TYPHFDLSHGAQV	2	0.9945	1
						TYPHFDLSHGAQV	2	0.9997	6
						TYPHFDLSHGAQV	4	0.9947	2
						VADALNAVAH	2	0.9585	1
						VADALNAVAH	2	0.9751	1
						VADALNAVAHVDDMPNALSALSDLHAHK	2	0.9362	1
						VADALNAVAHVDDMPNALSALSDLHAHK	3	0.9995	6
						VADALNAVAHVDDMPNALSALSDLHAHK	4	0.9858	1
						VGAHAGEYGA	2	0.8518	1
						VGAHAGEYGAEAL	2	0.988	2
						VGAHAGEYGAEALER	2	0.9997	7
						VGAHAGEYGAEALER	3	0.9996	6
						VGAHAGEYGAEALERM	2	0.9175	1
						VTLAAHLP	3	0.9861	4
						VTLAAHLP	4	0.9491	1
QS867-1	P78371	TCPB_HUMAN	CCT2	T-complex protein 1 subunit beta	1.0000	29.53	9	13	27
						AAHSEGNITAGLDMR	2	0.9985	1
						EGTIGDMAILGITSFQV	2	0.9996	4
						EGTIGDMAILGITSFQV	3	0.9857	3
						GATQQLDEAER	2	0.9992	3
						HGINCFINR	2	0.9822	1
						LTSFIGAIAIGDLVK	2	0.9997	3
						LTSFIGAIAIGDLVK	3	0.9959	2
						MLPTIADNAGYDSADLVQRL	3	0.961	1
						QLIYNYPEQLFGAAGVMAIEHADFAGVER	3	0.9992	3
						QVLLSAAEAEEVLR	2	0.9997	3
						QVLLSAAEAEEVLR	3	0.9352	1
						VQDDDEVGDGTTSTVTLAEALLR	2	0.9996	1
						VQDDDEVGDGTTSTVTLAEALLR	3	0.9103	1
QS868-1	P78371-2	TCPB_HUMAN	CCT2	Isoform 2 of T-complex protein 1 subunit beta	1.0000	2.46	1	1	3
						GATQQLDEAER	2	0.9992	3
QS869-1	P80188-2	NGAL_HUMAN	LCN2	Isoform 2 of Neutrophil gelatinase-associated lipocalin	1.0000	14.14	2	6	6
						VPLDQNFQDNQFOGK	2	0.9996	2
						VYVYVGLAGNAILR	2	0.9994	4
QS870-1	P80511	S10AC_HUMAN	S100A12	Protein S100-A12	1.0000	72.83	10	15	35
						AVIDEIQGLDANQDEQVDF	2	0.9397	1
						AVIDEIQGLDANQDEQVDFQEFISLVAIALK	3	0.9994	5
						AVIDEIQGLDANQDEQVDFQEFISLVAIALK	4	0.999	3
						DKAVIDEIQGLDANQDEQVDFQEFISLVAIALK	3	0.8865	1
						GHFDTLK	2	0.9979	1
						GHFDTLKSGELK	2	0.9895	2
						KGHFDTLKSGELK	2	0.9966	3
						KGHFDTLKSGELK	3	0.9782	1
						LEEHLGIVNIFH	2	0.9696	2
						LEEHLGIVNIFH	3	0.9406	2
						LEEHLGIVNIFHOY	2	0.9641	2
						LEEHLGIVNIFHOYSVR	3	0.9995	4
						LEEHLGIVNIFHOYSVR	4	0.9989	2
						TKLEEHLGIVNIFHOYSVR	3	0.9991	4
						TKLEEHLGIVNIFHOYSVR	4	0.9961	2
QS871-1	P80748	LV302_HUMAN		Ig lambda chain V-III region LOI	0.9214	14.41	1	1	1
						FSGNSGNTATLTISR	2	0.9214	1
QS872-1	P81605	DCD_HUMAN	DCD	Dermcidin	1.0000	25.45	2	3	5
						GAVHDVKDVLDSVL	2	0.9375	1
						LKDAVEDLESVGK	2	0.9991	2
						LKDAVEDLESVGK	3	0.9984	2
QS873-1	P81605-2	DCD_HUMAN	DCD	Isoform 2 of Dermcidin	1.0000	11.57	1	2	4
						LKDAVEDLESVGK	2	0.9991	2
						LKDAVEDLESVGK	3	0.9984	2
QS874-1	P98160	PGBM_HUMAN	HSPG2	Basement membrane-specific heparan sulfate proteoglycan	1.0000	6.01	19	19	31
						AELLQLVQLSEAVLIQTYNTK	3	0.9996	3
						AELLVTEAPSKPITVTEEQR	3	0.9822	1
						CAPGYGYNPSQGPCQR	2	0.9997	1
						CEQCQPGYVGDAQR	2	0.9997	1
						CLCLPGFSGPR	2	0.9098	1
						CRPVNQEIVR	2	0.996	2
						CSATGSPAPTHWSK	2	0.9981	2
						DFSLGLQDGHVFR	3	0.8136	1
						PHLMLALAGIOTLLIR	3	0.9896	2
						EVSEAVVDTLESEYK	2	0.9993	2
						LEGDTLIIPR	2	0.9994	1
						LLSGPYFWSLPSR	2	0.9984	3

						RGSIQVDGEELVSGR	2	0.9964	2
						RYQLGSGEAR	2	0.9124	1
						SIVPQGGSHSLR	2	0.9979	1
						SLPEVPETIELEVR	2	0.9994	3
						TCESLGAGGYR	2	0.9959	1
						TPSGLYGTCTER	2	0.9914	2
						YELGSLGLAVLR	2	0.9695	1
QS875-1	P98164	LRP2_HUMAN	LRP2	Low-density lipoprotein receptor-related protein 2	1.0000	0.92	3	3	5
						IFWPCGLTDYPPNR	2	0.9573	1
						NLYWTDYALETIEVSK	2	0.9995	3
						TVMSLDYDSVSDR	2	0.995	1
QS876-1	Q00577	PURA_HUMAN	PURA	Transcriptional activator protein Pur-alpha	0.9044	2.8	1	1	2
						FFFDVGSNK	2	0.9044	2
QS877-1	Q00610	CLH1_HUMAN	CLTC	Clathrin heavy chain 1	1.0000	13.43	15	15	25
QS877-2	Q00610-2	CLH1_HUMAN	CLTC	Isoform 2 of Clathrin heavy chain 1	1.0000	13.73	15	15	25
						CNEPAVWSQLAK	2	0.9732	1
						ESYVETLIFALAK	2	0.9997	2
						FQEHQLQLNLGINPANIGFSTLTMSDKFICIR	4	0.8683	1
						GQCDLELVNVCNENSLFK	2	0.9519	1
						HDVVLITK	2	0.9889	2
						HSSLAGCQINYYR	2	0.9779	1
						ISGETFVTAPHEATAGIGVNR	3	0.9988	2
						KFDVNTSAVQVLIHIGNLDR	3	0.9997	3
						LEKHEUEFR	3	0.8668	1
						LLPWLEAR	2	0.9975	2
						NLQNLULTAIK	2	0.9996	2
						NNLAGAEELFAR	2	0.9978	2
						TLQIFNIEMK	2	0.9701	2
						TSIDAYDNFDNISLAQR	2	0.999	1
						VGYPDWIFLLR	2	0.9992	2
QS878-1	Q01082-3	SPTB2_HUMAN	SPTBN1	Isoform 2 of Spectrin beta chain, non-erythrocytic 1	1.0000	2.51	4	4	8
QS878-2	Q01082-2	SPTB2_HUMAN	SPTBN1	Isoform Short of Spectrin beta chain, non-erythrocytic 1	1.0000	2.49	4	4	8
QS878-3	Q01082	SPTB2_HUMAN	SPTBN1	Spectrin beta chain, non-erythrocytic 1	1.0000	2.28	4	4	8
						DVEDELWVGER	2	0.9983	2
						EVDDLEQWIAER	2	0.9991	2
						HQILEQAVEDYAETHQLSK	3	0.9992	3
						LTLELLEVR	2	0.9973	1
QS879-1	Q01105-2	SET_HUMAN	SET	Isoform 2 of Protein SET	1.0000	29.5	6	6	17
QS879-2	Q01105-3	SET_HUMAN	SET	Isoform 3 of Protein SET	1.0000	30.83	6	6	17
QS879-3	Q01105-4	SET_HUMAN	SET	Isoform 4 of Protein SET	1.0000	30.48	6	6	17
QS879-4	Q01105	SET_HUMAN	SET	Protein SET	1.0000	28.28	6	6	17
						EFHLESQDPSSK	2	0.9994	2
						IDFYDENPYFENK	2	0.9997	3
						IPNFVWTFVFNHPQVSALLGEEDEALHYLTR	4	0.9974	3
						LROPFCKR	3	0.9708	1
						SGYRIDFYDENPYFENK	3	0.9971	4
						VEYTFEDIK	2	0.9997	4
QS880-1	Q01518	CAP1_HUMAN	CAP1	Adenylyl cyclase-associated protein 1	1.0000	20.84	8	8	14
QS880-2	Q01518-2	CAP1_HUMAN	CAP1	Isoform 2 of Adenylyl cyclase-associated protein 1	1.0000	20.89	8	8	14
						ALLVTASQCQPAENK	2	0.9997	3
						CVNTTLQIK	2	0.9544	1
						DVVGVEIINSK	2	0.9696	2
						LGLVFDVVGVGEIINSK	3	0.9989	1
						LSDLLAPISEKIEVITFR	3	0.9911	2
						NSLDCIEVSAR	2	0.9976	2
						VENQENSVNLVIEDTELK	2	0.9996	2
QS881-1	Q01813	PFKAP_HUMAN	PFKP	ATP-dependent 6-phosphofructokinase, platelet type	1.0000	VPTISNK	2	0.9823	1
QS881-2	Q01813-2	PFKAP_HUMAN	PFKP	Isoform 2 of ATP-dependent 6-phosphofructokinase, platelet	1.0000	4.34	3	3	4
						4.38	3	3	4
						DLSQSNVEHTEK	2	0.9994	2
						MLAIYDGFDFGFAK	2	0.9941	1
						VTILGHVQR	2	0.9978	1
QS882-1	Q01814	AT2B2_HUMAN	ATP2B2	Plasma membrane calcium-transporting ATPase 2	0.9931	3.22	2	2	2
						GLNRIQTQIR	3	0.9212	1
						KGDGLQLPAADGAAASNAADSANASLVNGK	3	0.912	1
QS883-1	Q02487	DSC2_HUMAN	DSC2	Desmocollin-2	0.9999	3.66	2	2	3
QS883-2	Q02487-2	DSC2_HUMAN	DSC2	Isoform 2B of Desmocollin-2	0.9999	3.9	2	2	3
						TSYVTSVEENTVDVEILR	2	0.999	2
						VTVEDKDLVNTANWR	3	0.9439	1
QS884-1	Q02763	TIE2_HUMAN	TEK	Angiotensin-1 receptor	0.9708	1.78	2	2	2
QS884-2	Q02763-2	TIE2_HUMAN	TEK	Isoform 2 of Angiotensin-1 receptor	0.9708	1.85	2	2	2
QS884-3	Q02763-3	TIE2_HUMAN	TEK	Isoform 3 of Angiotensin-1 receptor	0.9708	2.05	2	2	2
						CICPPGFMR	2	0.8247	1
						DGLRMDAAIK	2	0.8334	1
QS885-1	Q02790	FKBP4_HUMAN	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	1.0000	5.88	2	2	3
						AWDIAIATMK	2	0.9942	1
						FEIGEGENDLPYGLER	2	0.9988	2
QS886-1	Q04695	K1C17_HUMAN	KRT17	Keratin, type I cytoskeletal 17	1.0000	40.28	14	16	29
						ADLEMQIENLKEELAYLK	3	0.9467	1
						ADLEMQIENLKEELAYLKK	3	0.8421	1
						ALEEANTELEVK	2	0.9991	2
						ASLEGNAETFNK	2	0.9996	3
						CEMEQQNQIEYK	2	0.9997	2
						DAEDWFFSKTELNK	2	0.9953	2
						DYSQYR	2	0.9026	1
						EVATNSSELVQSGK	2	0.9997	2
						ILNEMRDQYKEK	2	0.9902	1
						ILTATVDNANILLQIDNAR	2	0.9995	3
						ILTATVDNANILLQIDNAR	3	0.999	2
						LSVEADINGLR	2	0.9783	1
						NHEEEMNALR	2	0.9996	2
						TKFETEQLR	2	0.9992	2
						TKFETEQLR	3	0.9955	1
QS887-1	Q04828	AK1C1_HUMAN	AKR1C1	Aldo-keto reductase family 1 member C1	1.0000	YCQLSQIGGUSVVEQLAQLR	3	0.9994	3
						18.39	9	10	22
						HIDSAHLYNNEEQVGLAIR	2	0.9997	3
						HIDSAHLYNNEEQVGLAIR	3	0.9996	5
						ILFDTVOLCATWEAVEK	2	0.9983	1
						LAIEAGFR	2	0.9995	2
						NLQLDYVDLYLHFPVSVPKPGEEVIPK	3	0.9978	2
						QNVQVFEFOLTSEEMK	2	0.9997	3
						REDIFYTSK	2	0.8377	1
						TPALIALR	2	0.9995	2
						TPALIALRY	2	0.9522	1
						YLTLDIFAGPPNYPFSDY	2	0.9953	2
QS888-1	Q04917	1433F_HUMAN	YWHAH	14-3-3 protein eta	1.0000	4.47	1	1	1
						YLAEVSSEK	2	0.8953	1
QS889-1	Q05519-2	SRSF11_HUMAN	SRSF11	Isoform 2 of Serine/arginine-rich splicing factor 11	1.0000	5.18	2	2	3
QS889-2	Q05519	SRSF11_HUMAN	SRSF11	Serine/arginine-rich splicing factor 11	1.0000	5.17	2	2	3
QS889-3	Q57760	Q57760_HUMAN	SRSF11	Serine/arginine-rich splicing factor 11 (Fragment)	1.0000	6.43	2	2	3
						ALIVVPYAEQVGPDEAK	2	0.9993	2
						TLFGFLGK	2	0.9783	1
QS890-1	Q06210	GFPT1_HUMAN	GFPT1	Glutamine-fructose-6-phosphate aminotransferase (isomer)	1.0000	5.01	2	2	4
QS890-2	Q06210-2	GFPT1_HUMAN	GFPT1	Isoform 2 of Glutamine-fructose-6-phosphate aminotransferase	1.0000	5.14	2	2	4
						AVEYFASDASAVIEHTNR	3	0.9877	1
						VIFLEDODDVAADVDR	2	0.9997	3
QS891-1	Q06481	APLP2_HUMAN	APLP2	Amyloid-like protein 2	1.0000	13.5	9	10	14
QS891-2	Q06481-3	APLP2_HUMAN	APLP2	Isoform 3 of Amyloid-like protein 2	1.0000	13.72	9	10	14
QS891-3	Q06481-6	APLP2_HUMAN	APLP2	Isoform 6 of Amyloid-like protein 2	1.0000	13.53	9	10	14
						CLVGEFYSVLLVPEK	2	0.9995	3
						CLVGEFYSVLLVPEK	3	0.9961	1
						FIYGGCGNR	2	0.9844	1
						LNMHVNIQTGK	2	0.9994	2

						LNMHVNIQTGKWEPTDPTGK	3	0.9986	2
						NNFESEDYCMVCK	2	0.9997	1
						VEAMLNDR	2	0.9958	1
						VPYVAQEIQEIIDELQEQR	2	0.995	1
						VSIDNWCR	2	0.9985	1
						WYFDLSK	2	0.9974	1
Q5892-1	Q06830	PRDX1_HUMAN	PRDX1	Peroxiredoxin-1	1.0000	9.55	2	0.997	3
						GLFIIDDK	2	0.9957	1
						QITVNDLPVGR	2	0.9982	2
Q5893-1	Q06945	SOX4_HUMAN	SOX4	Transcription factor SOX-4	0.9999	2.32	1	1	1
						LILAGGGGGK	2	0.9785	1
Q5894-1	Q07507	DERM_HUMAN	DPT	Dermatopontin	0.9729	8.46	1	1	1
						QGFSYQCPQGQVIVAVR	2	0.9729	1
Q5895-1	Q08211	DHX9_HUMAN	DHX9	ATP-dependent RNA helicase A	0.9993	0.94	2	2	6
Q5895-2	Q08211-2	DHX9_HUMAN	DHX9	Isoform 2 of ATP-dependent RNA helicase A	0.9993	5.11	2	2	6
						GAYGTGYFGQGR	2	0.964	1
						YGTGYFGQGR	2	0.9867	5
Q5896-1	Q08380	LG3BP_HUMAN	LGALS3BP	Galectin-3-binding protein	1.0000	9.4	3	4	9
						ALMLCEGLVADVITDFEGWK	2	0.9827	1
						ELSEALGGQFSOR	2	0.999	2
						GGWGTVCNWLWLTDAASVCCR	2	0.9997	4
						GGWGTVCNWLWLTDAASVCCR	3	0.9969	2
Q5897-1	Q12882	DPYD_HUMAN	DPYD	Dihydropyrimidine dehydrogenase [NADP(+)]	0.9457	0.88	1	1	1
						KNDWTELAK	2	0.9103	1
Q5898-1	Q12904	AIMP1_HUMAN	AIMP1	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	1.0000	10.26	3	3	4
Q5898-2	Q12904-2	AIMP1_HUMAN	AIMP1	Isoform 2 of Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	1.0000	9.52	3	3	4
						GAEADQIEYLK	2	0.9996	2
						IGCITAR	2	0.9987	1
						MVILLCNLPAK	3	0.9847	1
Q5899-1	Q12923-3	PTN13_HUMAN	PTPN13	Isoform 3 of Tyrosine-protein phosphatase non-receptor type 13	0.9909	1.54	2	2	2
Q5899-2	Q12923-4	PTN13_HUMAN	PTPN13	Isoform 4 of Tyrosine-protein phosphatase non-receptor type 13	0.9909	1.53	2	2	2
Q5899-3	Q12923	PTN13_HUMAN	PTPN13	Tyrosine-protein phosphatase non-receptor type 13	0.9909	1.53	2	2	2
						GDSMDIEATYSSQDHQTPK	2	0.9333	1
						RLSCSELVYQLQNSSK	2	0.8631	1
Q5900-1	Q13103	SPP24_HUMAN	SPP2	Secreted phosphoprotein 24	1.0000	9.95	2	2	3
						DALSASVVK	2	0.9825	1
						VNSQSLSPYLFR	2	0.9997	2
Q5901-1	Q13151	ROA0_HUMAN	HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	0.9816	5.25	1	1	3
						LFIGGLNVQTSSEGLR	2	0.9816	3
Q5902-1	Q13247-3	SRSF6_HUMAN	SRSF6	Isoform SRP55-3 of Serine/arginine-rich splicing factor 6	1.0000	9.55	4	4	5
Q5902-2	Q13247	SRSF6_HUMAN	SRSF6	Serine/arginine-rich splicing factor 6	1.0000	9.3	4	4	5
						CSWQDLK	2	0.993	1
						ILEVDLR	2	0.9731	1
						LVENLSR	2	0.9965	1
						TNSGVNER	2	0.9929	2
Q5903-1	Q13268	DHRS2_HUMAN	DHRS2	Dehydrogenase/reductase SDR family member 2, mitochondrial	1.0000	36.07	9	11	14
						AGVCHVGK	2	0.886	1
						LOGEGLSVAGVCHVGK	2	0.9979	1
						LOGEGLSVAGVCHVGK	3	0.9921	1
						LSVAGVCHVGK	2	0.9442	1
						SAGVNPVGVSTLTSEQIWOK	2	0.9922	1
						SPALLSQLLPYMENRR	3	0.9954	2
						TLALEAPK	2	0.9656	1
						VAVVTGSTSGIGFAIAR	2	0.9996	3
						VFHGNSLWK	2	0.9827	1
						VFHGNSLWK	3	0.8937	1
						VNCVQPGIK	2	0.9975	1
Q5904-1	Q13347	EIF3I_HUMAN	EIF3I	Eukaryotic translation initiation factor 3 subunit I	1.0000	11.08	3	3	6
						FHILAFEEFGR	3	0.9995	3
						IHYFDQVQFEFEFA	2	0.9992	2
						SGEVLNVVK	2	0.9973	1
Q5905-1	Q13509	TBB3_HUMAN	TUBB3	Tubulin beta-3 chain	1.0000	15.11	4	4	8
						ALTVPELTQQMFDAK	2	0.9994	4
						FWEVIDEHGIDGPSNGYVGDSDLQLER	3	0.9989	2
						MSSTFGNSTAIQELFK	2	0.9986	1
						YLTVAIVFR	2	0.992	1
Q5906-1	Q13510-3	ASAH1_HUMAN	ASAH1	Isoform 3 of Acid ceramidase	1.0000	19.02	6	6	11
						ESLDVVELDAK	2	0.9992	1
						GGFETVLR	2	0.9932	1
						LTVITLIDVTK	2	0.9997	3
						TSQENISFETMYDVLTSTKPVLNK	3	0.9988	3
						WKHPFLDDR	3	0.9442	2
						WVVVQTNVDR	2	0.9938	1
Q5907-1	Q13882-2	PTK6_HUMAN	PTK6	Isoform 2 of Protein-tyrosine kinase 6	0.9993	20.15	3	3	3
Q5907-2	Q13882	PTK6_HUMAN	PTK6	Protein-tyrosine kinase 6	0.9993	5.99	3	3	3
						AGDVFHVAR	2	0.9756	1
						SRTDELSFR	2	0.9647	1
						YVGLWDFK	2	0.9697	1
Q5908-1	Q13885	TBB2A_HUMAN	TUBB2A	Tubulin beta-2A chain	1.0000	26.07	7	7	12
						ALTVPELTQQMFDSK	2	0.9952	3
						ESESCDCLQGFQLTLSLGGGTSGMGTLISK	3	0.9946	1
						FWEVIDEHGIDGPSNGYVGDSDLQLER	3	0.9981	3
						INVYVNEAAGNK	2	0.9996	1
						INVYVNEAAGNKVYPR	3	0.8469	1
						MSATFGNSTAIQELFK	2	0.8786	1
						YLTVAIAIFR	2	0.9989	2
Q5909-1	Q13938-3	CAYP1_HUMAN	CAPS	Isoform 2 of Calyculin A	1.0000	37.04	5	5	8
						EAVIAAFAK	2	0.9987	1
						GASGIGLAR	2	0.9979	1
						LGLVLDQAEAGVCR	2	0.9997	2
						NGSGTLDLEFLR	2	0.9993	3
						SGDGVTVVDLRL	2	0.9981	1
Q5910-1	Q14117	DPY5_HUMAN	DPY5	Dihydropyrimidinase	0.9991	2.31	1	1	2
						GGSLIEAFETWR	2	0.9504	2
Q5911-1	Q14166	TTL12_HUMAN	TTL12	Tubulin-tyrosine ligase-like protein 12	1.0000	4.66	2	2	3
						DLDTGEEVTR	2	0.8342	1
						FTLTQSEADADILFNFSHK	3	0.9938	2
Q5912-1	Q14204	DYHC1_HUMAN	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	1.0000	5.32	18	18	22
						EGTEAWEAAMK	2	0.9135	1
						FGNPLLVQDVESYDPVLPVPLNR	3	0.9708	2
						FNYGFEYLGVDK	2	0.9986	1
						GIFEALRPLETLPVEGLIR	3	0.8999	1
						IQGLTVEQAEAVVR	2	0.9997	2
						KLVPILLEDGGEAPAALEALEEK	3	0.9215	1
						LALESICLLGESTTDWK	2	0.9406	1
						LLNTFLER	2	0.9648	1
						LVPLLEDGGEAPAALEALEEK	3	0.8355	1
						LVQPTLDR	2	0.9879	1
						REEFVQWVELLPDQTPQSWLGLPNNAER	3	0.9425	1
						TEYLSNADER	2	0.993	1
						TTDLTLDWEK	2	0.9817	1
						VQVALEELQDLK	2	0.9976	1
						VTFVNFVTR	2	0.9992	2
						WAIAGLNADMLK	2	0.9853	1
						YATLATVSR	2	0.9972	2
						YKEEYAVLISEAQAIK	3	0.9457	1
Q5913-1	Q14210	LY6D_HUMAN	LY6D	Lymphocyte antigen 6D	1.0000	11.72	1	1	2
						TINTVPLRGLNVKK	2	0.9855	2
Q5914-1	Q14258	TRIM25_HUMAN	TRIM25	E3 ubiquitin/ISG15 ligase TRIM25	0.9706	3.02	2	2	1
						TCSPASLSQASADLEATLR	2	0.9706	1
Q5915-1	Q14314	FGL2_HUMAN	FGL2	Fibroleukin	1.0000	29.16	12	14	26
						AGFGNLR	2	0.9978	1
						AKDVCPRLESR	2	0.9792	2

						CPSQEIQSRPVQHLYK	3	0.9535	2
						DCSDYIAIGKR	2	0.9995	1
						DVCPVRLESR	2	0.8333	1
						ELESEVNLSSLEK	2	0.9994	2
						GKCEEAGECPYQVSLPLTLQPK	3	0.9986	3
						IEEVFREYQNLK	2	0.9992	2
						IEEVFREYQNLK	3	0.9889	2
						LNLMNMNNIYVDSK	2	0.9997	3
						NAKEINVLUHR	2	0.9994	3
						NAKEINVLUHR	3	0.9994	2
						PVQHLYK	2	0.8937	1
						VRELESEVNLSSLEK	3	0.9755	1
Q5916-1	Q14376	GALE_HUMAN	GALE	UDP-glucose 4-epimerase	1.0000	20.4	8	8	15
						DLCQADKTWNAVLLR	3	0.9921	2
						DVIHVVDLAK	2	0.9993	4
						EGDVAACYANPSLAQEELGWTAALGLDR	3	0.9947	1
						FFIEEMIR	2	0.995	1
						MCEDLWR	2	0.9734	1
						REGDVAACYANPSLAQEELGWTAALGLDR	3	0.9994	4
						SKFFIEEMIR	3	0.976	1
						YANPSLAQEELGWTAALGLDR	2	0.9181	1
Q5917-1	Q14520	HABP2_HUMAN	HABP2	Hyaluronan-binding protein 2	1.0000	7.32	3	3	5
Q5917-2	Q14520-2	HABP2_HUMAN	HABP2	Isoform 2 of Hyaluronan-binding protein 2	1.0000	7.68	3	3	5
						FCEIGSDDCYVGDGYSYR	2	0.9996	1
						GQCLUTQSPYYR	2	0.9942	3
						LIANTLCNSR	2	0.9897	1
Q5918-1	Q14624-4	ITI4_HUMAN	ITI4	Isoform 4 of Inter-alpha-trypsin inhibitor heavy chain H4	1.0000	11.48	7	7	22
						AGFSWIEVTFK	2	0.9994	4
						ANTVQEATFQMLPK	2	0.9996	4
						DQFNLIVFSTEQWRPSLPVSAEENVK	3	0.9312	1
						ITFELVYELLK	2	0.9995	3
						LGIVYELLK	2	0.9995	3
						RLDYGQGPVGVSEICWSVEL	2	0.9995	5
						RLGIVYELLK	3	0.9989	2
Q5919-1	Q14764	MVP_HUMAN	MVP	Major vault protein	1.0000	17.81	12	13	18
						AQALAIETAEALQR	2	0.9997	2
						AQQLAEVEVKK	2	0.9832	1
						DAQGLVLDVTGQVR	2	0.9828	1
						ELELVYAR	2	0.9893	1
						ELLELEALSMAVESTGTAK	2	0.9582	1
						GPLEYVPSAK	2	0.9984	1
						HYCTVANPVS	2	0.9798	1
						IEGEGSVLQAK	2	0.9857	2
						KEVEVEIQATIR	2	0.9996	1
						KEVEVEIQATIR	3	0.9317	2
						LQDPFPLYPGEVLEK	2	0.9994	3
						QAIPIDENEGIVYODVK	2	0.9969	1
						TAVFGFETSEAK	2	0.9879	1
Q5920-1	Q14929	ZN169_HUMAN	ZN169	Zinc finger protein 169	0.9993	3.65	2	2	2
						EWKLLSQAQRTLYR	2	0.9865	1
						SSLFSHQK	2	0.949	1
Q5921-1	Q15075	EEA1_HUMAN	EEA1	Early endosome antigen 1	0.9995	2.27	3	3	3
						KLEADSLEVK	2	0.9449	1
						LSAETSLHR	2	0.9729	1
						LSAQEDLISNR	2	0.9835	1
Q5922-1	Q15149	PLEC_HUMAN	PLEC	Plectin	0.9998	0.45	2	2	3
						ISLETYNLLR	2	0.9846	2
						LTAEDLFEAR	2	0.8906	1
Q5923-1	Q15149-2	PLEC_HUMAN	PLEC	Isoform 2 of Plectin	0.9998	0.24	1	1	2
Q5923-2	Q15149-3	PLEC_HUMAN	PLEC	Isoform 3 of Plectin	0.9998	0.24	1	1	2
Q5923-3	Q15149-4	PLEC_HUMAN	PLEC	Isoform 4 of Plectin	0.9998	0.24	1	1	2
Q5923-4	Q15149-5	PLEC_HUMAN	PLEC	Isoform 5 of Plectin	0.9998	0.24	1	1	2
Q5923-5	Q15149-6	PLEC_HUMAN	PLEC	Isoform 6 of Plectin	0.9998	0.24	1	1	2
Q5923-6	Q15149-7	PLEC_HUMAN	PLEC	Isoform 7 of Plectin	0.9998	0.24	1	1	2
Q5923-7	Q15149-8	PLEC_HUMAN	PLEC	Isoform 8 of Plectin	0.9998	0.24	1	1	2
Q5923-8	Q15149-9	PLEC_HUMAN	PLEC	Isoform 9 of Plectin	0.9998	0.24	1	1	2
Q5924-1	Q15185-2	TEBP_HUMAN	PTGES3	Isoform 2 of Prostaglandin E synthase 3	1.0000	28.35	3	4	17
						DYVFIEFCVEDSKDVNNFEK	3	0.9931	4
						LTFSCLGSDNFK	2	0.9997	5
						SKLTFSCLGSDNFK	2	0.9995	5
						SKLTFSCLGSDNFK	3	0.9942	3
Q5925-1	Q15185-3	TEBP_HUMAN	PTGES3	Isoform 3 of Prostaglandin E synthase 3	1.0000	27.69	4	5	21
Q5925-2	Q15185-4	TEBP_HUMAN	PTGES3	Isoform 4 of Prostaglandin E synthase 3	1.0000	25.9	4	5	21
Q5925-3	Q15185	TEBP_HUMAN	PTGES3	Prostaglandin E synthase 3	1.0000	22.5	4	5	21
						DYVFIEFCVEDSK	2	0.9993	4
						DYVFIEFCVEDSKDVNNFEK	3	0.9931	4
						LTFSCLGSDNFK	2	0.9997	5
						SKLTFSCLGSDNFK	2	0.9995	5
						SKLTFSCLGSDNFK	3	0.9942	3
Q5926-1	Q15323	K1H1_HUMAN	KRT31	Keratin, type I cellular Ha1	1.0000	6.01	2	2	4
						DSLENTTESGAR	2	0.9983	2
						QINQEQVLLDVR	2	0.9907	2
Q5927-1	Q15365	PCBP1_HUMAN	PCBP1	Poly(rC)-binding protein 1	0.9995	6.18	2	2	3
						IANPVGSSGR	2	0.8206	1
						INISEGNCPCR	2	0.9946	2
Q5928-1	Q15485	FCN2_HUMAN	FCN2	Ficolin-2	1.0000	19.49	6	10	23
Q5928-2	Q15485-2	FCN2_HUMAN	FCN2	Isoform 2 of Ficolin-2	1.0000	22.18	6	10	23
						LGFWLGNNDNIHALTAQGTSELR	2	0.9997	2
						LGFWLGNNDNIHALTAQGTSELR	3	0.9997	4
						RVDGSDVDFYR	2	0.9996	3
						RVDGSDVDFYR	3	0.9947	1
						RVDGSDVDFYROWATYK	2	0.9881	2
						RVDGSDVDFYROWATYK	3	0.9678	1
						TCQDLDR	2	0.9985	2
						VDGSDVDFYR	2	0.9198	1
						VDLVDFEDNYQFAK	2	0.9998	6
						VDLVDFEDNYQFAK	3	0.9949	1
Q5929-1	Q16204	CCDC6_HUMAN	CCDC6	Coiled-coil domain-containing protein 6	0.9765	2.95	1	1	2
						AEQEEFISNTLFK	2	0.9765	2
Q5930-1	Q16772	GSTA3_HUMAN	GSTA3	Glutathione S-transferase A3	1.0000	9.91	2	2	9
						AILNYIAK	2	0.9966	1
						WLLAAGVEFEK	2	0.9997	8
Q5931-1	Q6F113	H2AZA_HUMAN	HIST2H2AA3	Histone H2A type 2-A	0.9960	22.31	1	1	1
Q5931-2	Q16777	H2AZC_HUMAN	HIST2H2AC	Histone H2A type 2-C	0.9960	22.48	1	1	1
						VGAGAPVYMAAVLEYLTAEILEAGNAAR	3	0.9931	1
Q5932-1	Q16787-3	LAMA3_HUMAN	LAMA3	Isoform 3 of Laminin subunit alpha-3	0.9994	0.95	2	2	2
Q5932-2	Q16787	LAMA3_HUMAN	LAMA3	Laminin subunit alpha-3	0.9994	0.93	2	2	2
						FGGSCQPCSCNSNGQLGSCHP	2	0.8996	1
						LHVEGPTCSR	2	0.9941	1
Q5933-1	Q562R1	ACTBL_HUMAN	ACTBL2	Beta-actin-like protein 2	1.0000	6.91	2	2	3
						IIAPPERK	2	0.9994	2
						VAPDEHPILLTEAPLNPK	3	0.9879	1
Q5934-1	Q58F6	H90B4_HUMAN	HSP90AB4P	Putative heat shock protein HSP 90-beta 4	1.0000	3.96	1	1	1
						GFEVYIMSEPIDYCVQQLK	3	0.8937	1
Q5935-1	Q5JR95	Q5JR95_HUMAN	RPS8	40S ribosomal protein S8	1.0000	22.87	4	5	8
						ADGVYLEGK	2	0.9985	1
						ELEFYLR	2	0.9757	1
						IIDVYVYASNNELVR	2	0.9997	2
						IIDVYVYASNNELVR	3	0.9908	2
						NCIVLDSTPYR	2	0.999	2
Q5936-1	Q5IRR9	Q5IRR9_HUMAN	UBA1	Ubiquitin-like modifier-activating enzyme 1 (Fragment)	1.0000	4.44	1	1	2
Q5936-2	Q5IR50	Q5IR50_HUMAN	UBA1	Ubiquitin-like modifier-activating enzyme 1 (Fragment)	1.0000	4.23	1	1	2

Q5936-3	Q5JRS1	Q5JRS1_HUMAN	UBA1	Ubiquitin-like modifier-activating enzyme 1 (Fragment)	1.0000	6.94	1	1	2
Q5936-4	Q5JRS2	Q5JRS2_HUMAN	UBA1	Ubiquitin-like modifier-activating enzyme 1 (Fragment)	1.0000	5.13	1	1	2
Q5936-5	Q5JRS3	Q5JRS3_HUMAN	UBA1	Ubiquitin-like modifier-activating enzyme 1 (Fragment)	1.0000	6.15	1	1	2
Q5937-1	Q5JV98	Q5JV98_HUMAN	STK24	Serine/threonine-protein kinase 24 12 kDa subunit (Fragment)	1.0000	LQTS5VLVSLGR	2	0.9989	2
						29.19	4	5	11
						ADIWSLGTAEIAR	2	0.9997	3
						ADIWSLGTAEIAR	3	0.9996	2
						GATYLAEEACPGISDTMVAQLVQR	3	0.9952	2
Q5938-1	Q5QPP4	Q5QPP4_HUMAN	GALE	UDP-glucose 4-epimerase (Fragment)	1.0000	SQACGGNLGSIEELR	2	0.9997	3
						VLFLIPK	2	0.9889	1
						26.78	7	7	14
						DLCAQDKTWNVAHLR	3	0.9921	2
						DYHVVDLAK	2	0.9993	4
Q5939-1	Q5QPP9	Q5QPP9_HUMAN	GALE	UDP-glucose 4-epimerase (Fragment)	1.0000	EGDVAACYANPSLAQEELGWTAALGLDR	3	0.9947	1
						FFIEEMIR	2	0.995	1
						REGDVAACYANPSLAQEELGWTAALGLDR	3	0.9994	4
						SKFFIEEMIR	3	0.976	1
						YANPSLAQEELGWTAALGLDR	2	0.9181	1
Q5940-1	Q5SQ12	Q5SQ12_HUMAN	PTGDS	Prostaglandin-H2 D-isomerase	1.0000	36.11	3	3	9
						DYHVVDLAK	2	0.9993	4
						EGDVAACYANPSLAQEELGWTAALGLDR	3	0.9947	1
						REGDVAACYANPSLAQEELGWTAALGLDR	3	0.9994	4
						10	1	1	2
Q5940-2	Q5SQ11	Q5SQ11_HUMAN	PTGDS	Prostaglandin-H2 D-isomerase (Fragment)	1.0000	8.21	1	1	2
Q5941-1	Q5STZ7	Q5STZ7_HUMAN	ABCF1	ATP-binding cassette sub-family F member 1	1.0000	TMLLQPGSLGSYSYR	2	0.9973	2
						10.5	2	2	2
						FGLESHAHTIQICK	3	0.9329	1
						GAVIVVSHDAR	2	0.9994	1
						7.41	3	3	5
Q5942-1	Q5SZU1	Q5SZU1_HUMAN	PHGDH	D-3-phosphoglycerate dehydrogenase	1.0000	AGTGVDNVDELEATR	2	0.9994	2
						GGIVDEGALLR	2	0.999	1
						VTADVMAAEK	2	0.9972	2
						16.28	2	2	5
						16.83	2	2	5
Q5943-1	Q5TOR1	Q5TOR1_HUMAN	CAP1	Adenyllyl cyclase-associated protein (Fragment)	1.0000	17.24	2	2	5
Q5943-2	Q5TOR2	Q5TOR2_HUMAN	CAP1	Adenyllyl cyclase-associated protein (Fragment)	1.0000	17.41	2	2	5
Q5943-3	Q5TOR3	Q5TOR3_HUMAN	CAP1	Adenyllyl cyclase-associated protein (Fragment)	1.0000	19.55	2	2	5
Q5943-4	Q5TOR4	Q5TOR4_HUMAN	CAP1	Adenyllyl cyclase-associated protein (Fragment)	1.0000	19.89	2	2	5
Q5943-5	Q5TOR5	Q5TOR5_HUMAN	CAP1	Adenyllyl cyclase-associated protein (Fragment)	1.0000	20.11	2	2	5
Q5943-6	Q5TOR6	Q5TOR6_HUMAN	CAP1	Adenyllyl cyclase-associated protein (Fragment)	1.0000	13.36	2	2	5
Q5943-7	Q5TOR7	Q5TOR7_HUMAN	CAP1	Adenyllyl cyclase-associated protein (Fragment)	1.0000				
Q5943-8	Q5TOR9	Q5TOR9_HUMAN	CAP1	Adenyllyl cyclase-associated protein (Fragment)	1.0000				
Q5944-1	Q5T457	UBR4_HUMAN	UBR4	E3 ubiquitin-protein ligase UBR4	0.9445	ALLVTASQCQPAENK	2	0.9997	3
						LSDLLAPISSEKIVETFR	3	0.9911	2
						0.23	1	1	2
						0.23	1	1	2
						0.23	1	1	2
Q5944-2	Q5T457-2	UBR4_HUMAN	UBR4	Isoform 2 of E3 ubiquitin-protein ligase UBR4	0.9445	0.23	1	1	2
Q5944-3	Q5T457-3	UBR4_HUMAN	UBR4	Isoform 3 of E3 ubiquitin-protein ligase UBR4	0.9445	0.23	1	1	2
Q5944-4	Q5T457-4	UBR4_HUMAN	UBR4	Isoform 4 of E3 ubiquitin-protein ligase UBR4	0.9445	0.23	1	1	2
Q5944-5	Q5T457-5	UBR4_HUMAN	UBR4	Isoform 5 of E3 ubiquitin-protein ligase UBR4	0.9445	0.49	1	1	2
Q5945-1	Q5T6L6	Q5T6L6_HUMAN	ASS1	Argininosuccinate synthase (Fragment)	1.0000	QLLQLLTYIVR	2	0.9445	2
						18.18	3	3	7
						FELSCYSLAPQIK	2	0.9997	3
						KVFIEDVSR	2	0.9952	2
						YLLGTSLARPCJAR	2	0.9971	2
Q5946-1	Q5T7D5	Q5T7D5_HUMAN	ALDOB	Fructose-bisphosphate aldolase	1.0000	14.8	2	2	5
						IADQCPSSLAIQENANALAR	2	0.9996	3
						LDQGGAPLAGTNK	2	0.9992	2
						6.81	1	1	2
						AGVNTVTVLENK	2	0.999	2
Q5947-1	Q5T8U3	Q5T8U3_HUMAN	RPL7A	60S ribosomal protein L7a (Fragment)	0.9999	12.24	2	2	4
						TEVNVLPQAK	2	0.9993	2
						VVNSSPQPNVVFQVQPK	2	0.9996	2
						3.5	6	6	10
						3.35	6	6	10
Q5948-1	Q5T987	Q5T987_HUMAN	ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2 (Fragment)	1.0000	ALEATTEHR	2	0.999	2
						ALSTDPAAPNLK	2	0.847	1
						AVSSAIAQLLGEVAGQNGENYAGIAR	3	0.9902	2
						GLAGAVSELLR	2	0.9994	2
						LAQAQSSVATITR	2	0.9992	2
Q5949-1	Q5T987	Q5T987_HUMAN	ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2 (Fragment)	1.0000	VLVQNAAGSQEK	2	0.9744	1
						2.98	3	3	4
						3	3	3	4
						3.77	3	3	4
						3.52	3	3	4
Q5950-1	Q9HC66-2	ARGAL_HUMAN	ARHGEF10L	Isoform 2 of Rho guanine nucleotide exchange factor 10-like	1.0000	2.89	3	3	4
Q5950-2	Q9HC66-3	ARGAL_HUMAN	ARHGEF10L	Isoform 3 of Rho guanine nucleotide exchange factor 10-like	1.0000	3	3	3	4
Q5950-3	Q9HC66-4	ARGAL_HUMAN	ARHGEF10L	Isoform 4 of Rho guanine nucleotide exchange factor 10-like	1.0000	3.77	3	3	4
Q5950-4	Q5VX14	Q5VX14_HUMAN	ARHGEF10L	Rho guanine nucleotide exchange factor 10-like protein	1.0000	3.52	3	3	4
Q5950-5	Q9HC66	ARGAL_HUMAN	ARHGEF10L	Rho guanine nucleotide exchange factor 10-like protein	1.0000	2.89	3	3	4
Q5951-1	Q5VYL6	Q5VYL6_HUMAN	CFHR5	Complement factor H-related protein 5	1.0000	EICSVAIISGGQGYR	2	0.9994	2
						NFGSALGSSGR	2	0.9838	1
						SPGLQPVLCRL	2	0.9969	1
						2.19	1	1	2
						2.28	1	1	2
Q5951-2	Q9BRX6	FHR5_HUMAN	CFHR5	Complement factor H-related protein 5	1.0000	ITCTEEGWSPTPK	2	0.9991	2
Q5952-1	Q66LE6	2ABD_HUMAN	PPP2R2D	Serine/threonine-protein phosphatase 2A 55 kDa regulatory	1.0000	2.43	1	1	2
						INLWHEITDR	2	0.9972	2
						23.38	2	2	5
						VHLVGDIDFTGK	3	0.9992	2
						YDCGEEILTVLSAMTEAAVAIK	3	0.9996	3
Q5954-1	Q6K866-2	K2C80_HUMAN	KRT80	Isoform 2 of Keratin, type II cytoskeletal 80	1.0000	2.13	1	1	1
Q5954-2	Q6K866-3	K2C80_HUMAN	KRT80	Isoform 3 of Keratin, type II cytoskeletal 80	1.0000	1.85	1	1	1
Q5954-3	Q6K866	K2C80_HUMAN	KRT80	Keratin, type II cytoskeletal 80	1.0000	1.99	1	1	1
Q5955-1	Q6M2W2	FSTL4_HUMAN	FSTL4	Follistatin-related protein 4	1.0000	KLVEGEGR	2	0.8984	1
						6.06	3	3	7
						7.58	3	3	7
						SFTESNQNYIAALHTPEDDLFLFELSTGK	3	0.9984	3
						VLVVDIOAQK	2	0.9961	2
Q5956-1	Q6P9A2	GLT18_HUMAN	GALNT18	Polypeptide N-acetylglucosaminyltransferase 18	0.9705	YEDTGATYCIK	2	0.9997	2
						1.98	1	1	3
						SPALIGCFVDR	2	0.9705	3
						15.73	5	6	7
						EPVGLQVAPLPLGTGALR	2	0.9926	1
Q5957-1	Q6PC80	VWA1_HUMAN	VWA1	von Willebrand factor A domain-containing protein 1	1.0000	EQLFAEASGARPVPK	2	0.9951	1
						GNFLESAASAPAEK	2	0.9977	1
						HLHFVDVDDLHIHQELR	3	0.9786	1
						HLHFVDVDDLHIHQELR	4	0.9864	2
						VREVGQVAPLPLGTGALR	3	0.9076	1
Q5958-1	Q6ZNA5	FRRS1_HUMAN	FRRS1	Ferric-chelate reductase 1	0.9018	6.25	1	1	1
Q5958-2	Q6ZNA5-2	FRRS1_HUMAN	FRRS1	Isoform 2 of Ferric-chelate reductase 1	0.9018	5.91	1	1	1
Q5959-1	Q7Q9C8-2	VP13C_HUMAN	VP513C	Isoform 2 of Vacuolar protein sorting-associated protein 13C	0.9728	NAEDLNGPPISFTLIDSEVSLTTCEDIQGSVSHR	3	0.9018	1
						0.3	1	1	1
						0.3	1	1	1
						0.31	1	1	1
						0.29	1	1	1
Q5959-2	Q7Q9C8-3	VP13C_HUMAN	VP513C	Isoform 3 of Vacuolar protein sorting-associated protein 13C	0.9728	0.31	1	1	1
Q5959-3	Q7Q9C8-4	VP13C_HUMAN	VP513C	Isoform 4 of Vacuolar protein sorting-associated protein 13C	0.9728	0.29	1	1	1
Q5959-4	Q7Q9C8	VP13C_HUMAN	VP513C	Vacuolar protein sorting-associated protein 13C	0.9728	TLDEVNIIAR	2	0.9728	1
Q5960-1	Q7QCQ4	UBP31_HUMAN	USP31	Ubiquitin carboxyl-terminal hydrolase 31	0.9002	0.74	1	1	1
						LSSPTQTAAK	2	0.8244	1
						8.18	2	2	2
						10.16	2	2	2
						DVGSDFDFELPLYK	2	0.9991	1
Q5961-1	Q7LSL3	GDPD3_HUMAN	GDPD3	Glycerophosphodiester phosphodiesterase domain-containing	1.0000	SOLLEDCQLTR	2	0.9942	1
Q5961-2	Q7LSL3-1	GDPD3_HUMAN	GDPD3	Isoform 2 of Glycerophosphodiester phosphodiesterase domain-containing	1.0000	54.95	9	9	48
Q5962-1	Q7Z5L0	VMO1_HUMAN	VMO1	Vitelline membrane outer layer protein 1 homolog	1.0000	CSOGEELOGPGLSWGDFGWDSDHCPK	3	0.9995	11
						GGNVLVASLR	2	0.9997	5
						GLGGDTALNDAR	2	0.9977	8
						GNVLGNTHVVE	2	0.8715	1
						GNVLGNTHVVE	2	0.8539	2
Q5962-2	Q7Z5L0	VMO1_HUMAN	VMO1	Vitelline membrane outer layer protein 1 homolog	1.0000	GNVLGNTHVVE	2	0.8509	1
						GNVLGNTHVVE	2	0.8509	1
						GNVLGNTHVVE	2	0.8509	1
						GNVLGNTHVVE	2	0.8509	1
						GNVLGNTHVVE	2	0.8509	1

						GNVLGNTHVVESQSGSGWGEWSEPLWCR	3	0.9997	8
						VEAPPTLGDNTAANNVR	2	0.9997	4
						VEPPQGIPIGDDTALNGIR	2	0.9991	8
Q5963-1	Q7Z794	K2C1B_HUMAN	KRT77	Keratin, type II cytoskeletal 1b	1.0000	4.33	1	1	1
						RVYSTSSAGSGGGSPAVGVCYAR	2	0.9637	1
Q5964-1	Q86UJ0	BCL9L_HUMAN	BCL9L	B-cell CLL/lymphoma 9-like protein	0.9126	0.6	1	1	1
Q5964-2	Q86UJ0-2	BCL9L_HUMAN	BCL9L	Isoform 2 of B-cell CLL/lymphoma 9-like protein	0.9126	0.6	1	1	1
Q5964-3	Q86UJ0-3	BCL9L_HUMAN	BCL9L	Isoform 3 of B-cell CLL/lymphoma 9-like protein	0.9126	0.65	1	1	1
Q5964-4	Q86UJ0-4	BCL9L_HUMAN	BCL9L	Isoform 4 of B-cell CLL/lymphoma 9-like protein	0.9126	0.62	1	1	1
						GLLSPPMGQ	2	0.8579	1
Q5965-1	Q86VP6	CAND1_HUMAN	CAND1	Cullin-associated NEDD8-dissociated protein 1	1.0000	9.51	11	12	16
						AADIDQEVK	2	0.996	1
						AADIDQEVKER	2	0.9589	1
						ADVFHAYLSLK	2	0.9973	1
						ADVFHAYLSLK	3	0.999	2
						FMAINDLMTLQK	2	0.9978	1
						ITSEALLVTQQLVK	2	0.9989	2
						LGTLSALDILK	2	0.9981	1
						LTLDIPETLLPR	2	0.9917	2
						NOGQDFK	2	0.981	1
						NGEVQNLAVK	2	0.9619	2
						SVLEAFSSPSEVK	2	0.9986	1
						TLEDPLNVR	2	0.9907	1
Q5966-1	Q86VQ1	GLC1_HUMAN	GLCC1	Glucocorticoid-induced transcript 1 protein	0.9623	6.22	1	1	1
						SAAGSPPAVAAGSGNGAGGGGVCAPAGAGR	3	0.8202	1
Q5967-1	Q8IYD1	ERF3B_HUMAN	GSPT2	Eukaryotic peptide chain release factor GTP-binding subunit 6	1.0000	5.89	3	3	3
						ETWYLSWALDTNQEER	2	0.9474	1
						HFTILDAPGHK	3	0.998	1
						KGEFTGFEK	2	0.9855	1
Q5968-1	Q8N111	CEND_HUMAN	CEND1	Cell cycle exit and neuronal differentiation protein 1	0.9051	12.75	1	1	1
						GPGDGAEEDEAASGGPGGR	2	0.9051	1
Q5969-1	Q8N159	NAGS_HUMAN	NAGS	N-acetylglutamate synthase, mitochondrial	0.9973	3.19	2	2	2
						ATALMANVLR	2	0.9579	1
						FVYSSSR	2	0.9349	1
Q5970-1	Q8N1G4	LRC47_HUMAN	LRRCA47	Leucine-rich repeat-containing protein 47	1.0000	3.95	2	2	4
						ELLTTPGLEER	2	0.9981	2
						TAATLATHELR	2	0.9931	2
Q5971-1	Q8N475	FSTL5_HUMAN	FSTL5	Follistatin-related protein 5	1.0000	1.3	1	1	1
Q5971-2	Q8N475-2	FSTL5_HUMAN	FSTL5	Isoform 2 of Follistatin-related protein 5	1.0000	1.3	1	1	1
Q5971-3	Q8N475-3	FSTL5_HUMAN	FSTL5	Isoform 3 of Follistatin-related protein 5	1.0000	1.31	1	1	1
						VIRVYPESQAR	2	0.8164	1
Q5972-1	Q8NCH7	Q8NCH7_HUMAN	ANGPTL2	Angiotensin-like 2, isoform CRA_c	1.0000	41.88	7	9	14
						HDPPGGWTVIQR	2	0.9781	1
						KVFAEYASFR	2	0.9975	1
						KVFAEYASFR	3	0.9943	2
						LGSGVNFRR	2	0.9986	2
						LLVTMEDWWSGR	2	0.9996	2
						QGFGNIDGEYWLGENIYVLTNQGNKY	3	0.9522	1
						RLDGSVNFRR	2	0.9979	2
						RLDGSVNFRR	3	0.9979	2
						YQDGVVWAEFR	2	0.9353	1
Q5973-1	Q8ND23	LR16B_HUMAN	LRRCA16B	Leucine-rich repeat-containing protein 16B	0.9961	1.24	2	2	3
						LESVASEVSK	3	0.8017	1
						RAQSCDK	2	0.9801	2
Q5974-1	Q8NFC6	BOD11_HUMAN	BOD11	Biorientation of chromosomes in cell division protein 1-like 1	0.9891	1.08	2	2	2
						RNENSEVDTAGSGSGAPSVLHQR	3	0.8848	1
						VKDSIDVERR	2	0.905	1
Q5975-1	Q8NFI4	F10A5_HUMAN	ST13P5	Putative protein FAM10A5	1.0000	6.23	2	2	5
						AIDLTDIAK	2	0.9861	2
						AIENIPDSAQPKY	2	0.9955	3
Q5976-1	Q8TE77	SSH3_HUMAN	SSH3	Protein phosphatase Slingshot homolog 3	1.0000	6.37	3	3	4
						IFPHLYLGESEWNAANLEELQR	3	0.8843	1
						QLQIYQGLTASR	2	0.9967	2
						YLLVSTR	2	0.9988	1
Q5977-1	Q8TE77-2	SSH3_HUMAN	SSH3	Isoform 2 of Protein phosphatase Slingshot homolog 3	1.0000	6.16	2	2	2
						IFPHLYLGESEWNAANLEELQR	3	0.8843	1
						YLLVSTR	2	0.9988	1
Q5978-1	Q8WUM4-2	PDC6I_HUMAN	PDC6IP	Isoform 2 of Programmed cell death 6-interacting protein	0.9996	1.26	1	1	3
Q5978-2	Q8WUM4	PDC6I_HUMAN	PDC6IP	Programmed cell death 6-interacting protein	0.9996	1.27	1	1	3
						FYNLELTYLR	2	0.998	3
Q5979-1	Q8WXI4	ACOT11_HUMAN	ACOT11	Acyl-coenzyme A thioesterase 11	1.0000	7.08	4	4	6
						GELSVGQLLK	2	0.9972	1
						RGETLCSGFCLWR	3	0.9927	1
						SVTLPTH	2	0.9655	1
						WIDTTACLSAER	2	0.9993	3
Q5980-1	Q8WXI4-2	ACOT11_HUMAN	ACOT11	Isoform 2 of Acyl-coenzyme A thioesterase 11	1.0000	11.11	6	6	9
						ACEQFLDNR	2	0.9904	2
						DNWVLSSEISQVR	2	0.9986	1
						GELSVGQLLK	2	0.9972	1
						RGETLCSGFCLWR	3	0.9927	1
						SVTLPTH	2	0.9655	1
						WIDTTACLSAER	2	0.9993	3
Q5981-1	Q8WX55	CCG8_HUMAN	CACNG8	Voltage-dependent calcium channel gamma-8 subunit	0.9659	11.29	1	1	1
						DPSKGSVAAGLAGAGGGGGGAVGAGGAAGAGGGGGGGGAGAGADR	3	0.9166	1
Q5982-1	Q8WZ42-10	TITIN_HUMAN	TTN	Isoform 10 of Titin	0.9949	0.07	2	2	2
Q5982-2	Q8WZ42-11	TITIN_HUMAN	TTN	Isoform 11 of Titin	0.9949	0.06	2	2	2
Q5982-3	Q8WZ42-12	TITIN_HUMAN	TTN	Isoform 12 of Titin	0.9949	0.06	2	2	2
Q5982-4	Q8WZ42-13	TITIN_HUMAN	TTN	Isoform 13 of Titin	0.9949	0.06	2	2	2
Q5982-5	Q8WZ42-2	TITIN_HUMAN	TTN	Isoform 2 of Titin	0.9949	0.06	2	2	2
Q5982-6	Q8WZ42-3	TITIN_HUMAN	TTN	Isoform 3 of Titin	0.9949	0.07	2	2	2
Q5982-7	Q8WZ42-4	TITIN_HUMAN	TTN	Isoform 4 of Titin	0.9949	0.06	2	2	2
Q5982-8	Q8WZ42-5	TITIN_HUMAN	TTN	Isoform 5 of Titin	0.9949	0.06	2	2	2
Q5982-9	Q8WZ42-7	TITIN_HUMAN	TTN	Isoform 7 of Titin	0.9949	0.06	2	2	2
Q5982-10	Q8WZ42-8	TITIN_HUMAN	TTN	Isoform 8 of Titin	0.9949	0.06	2	2	2
Q5982-11	Q8WZ42-9	TITIN_HUMAN	TTN	Isoform 9 of Titin	0.9949	0.07	2	2	2
Q5982-12	Q8WZ42	TITIN_HUMAN	TTN	Titin	0.9949	0.06	2	2	2
						KSAATSLEK	2	0.917	1
						LITTCCEVVPN	2	0.8425	1
Q5983-1	Q8WZ75-2	ROBO4_HUMAN	ROBO4	Isoform 2 of Roundabout homolog 4	1.0000	3.64	3	3	5
Q5983-2	Q8WZ75	ROBO4_HUMAN	ROBO4	Roundabout homolog 4	1.0000	3.38	3	3	5
						LSVAVLR	2	0.9975	1
						LSVAVLREDFQIQPR	3	0.997	2
						VSQEPQDYTEVELLAVR	2	0.9992	2
Q5984-1	Q92499	DDX1_HUMAN	DDX1	ATP-dependent RNA helicase DDX1	0.9999	4.32	2	3	4
						ELLIGGVAAR	2	0.9969	1
						FLVLDEADGLLSQGYSDFINR	2	0.9888	1
						FLVLDEADGLLSQGYSDFINR	3	0.9929	2
Q5985-1	Q92598-3	HS105_HUMAN	HSPH1	Isoform 3 of Heat shock protein 105 kDa	1.0000	3.43	2	2	5
						AGGIETIANEFSOR	2	0.9994	3
						GCALDCAILSPAFAK	2	0.9991	2
Q5986-1	Q92598	HS105_HUMAN	HSPH1	Heat shock protein 105 kDa	1.0000	5.01	2	2	4
Q5986-2	Q92598-2	HS105_HUMAN	HSPH1	Isoform Beta of Heat shock protein 105 kDa	1.0000	5.28	2	2	4
						AGGIETIANEFSOR	2	0.9994	3
						LKETAENSLKKPYTDCVISVPSFTDAER	3	0.851	1
Q5987-1	Q92688	AN32B_HUMAN	ANP32B	Acidic leucine-rich nuclear phosphoprotein 32 family member 1	1.0000	26.69	5	6	11
Q5987-2	Q92688-2	AN32B_HUMAN	ANP32B	Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member 1	1.0000	34.36	5	6	11
						ELVDNCK	2	0.9745	1
						KLLESENK	2	0.99	2
						LELESENK	2	0.9104	1
						SLDFNCEVTNLDNYR	2	0.9997	4
						SLDFNCEVTNLDNYR	3	0.9929	2
						SNQDKIEGLTAEFVNLEFLSUNVLGIVSNLPK	3	0.9679	1
Q5988-1	Q92820	GGH_HUMAN	GGH	Gamma-glutamyl hydrolase	1.0000	33.65	9	11	20

						KPIGILMQK	2	0.9975	1
						KPIGILMQK	3	0.9993	1
						LDLTEKDYELFK	2	0.9988	2
						LDLTEKDYELFK	3	0.9926	2
						MFQNFPTTELLSLAVEPLTANFHK	3	0.9791	1
						NLDGSHAPNAVK	2	0.9997	4
						RLDLTEKDYELFK	3	0.8465	1
						SINGILFPGSGVDLR	2	0.9982	2
						TAFYLAFFVNEAR	3	0.9996	3
						YLESAGAR	2	0.934	1
						YYIAASYVK	2	0.9997	2
Q5989-1	Q92882	OSTF1_HUMAN	OSTF1	Osteoclast-stimulating factor 1	1.0000	5.61	1	1	2
						GYADIVQLLLAK	2	0.9995	2
Q5990-1	Q93084-2	AT2A3_HUMAN	ATP2A3	Isoform SERCA3A of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	1.0000	1.5	1	1	2
Q5990-2	Q93084-3	AT2A3_HUMAN	ATP2A3	Isoform SERCA3C of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	1.0000	1.46	1	1	2
Q5990-3	Q93084-6	AT2A3_HUMAN	ATP2A3	Isoform SERCA3D of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	1.0000	1.44	1	1	2
Q5990-4	Q93084-5	AT2A3_HUMAN	ATP2A3	Isoform SERCA3E of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	1.0000	1.43	1	1	2
Q5990-5	Q93084-7	AT2A3_HUMAN	ATP2A3	Isoform SERCA3F of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	1.0000	1.45	1	1	2
Q5990-6	Q93084-4	AT2A3_HUMAN	ATP2A3	Isoform SERCA3G of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	1.0000	1.5	1	1	2
Q5990-7	Q93084	AT2A3_HUMAN	ATP2A3	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	1.0000	1.44	1	1	2
						VGEATETALTCLVEK	2	0.9992	2
Q5991-1	Q96A08	H2B1A_HUMAN	HIST1H2BA	Histone H2B type 1-A	1.0000	7.09	1	1	2
						LLLPGLAK	2	0.9986	2
Q5992-1	Q96818	DACT3_HUMAN	DACT3	Dapper homolog 3	0.9921	5.41	2	2	3
						RGAGQPTSPGGADGGPR	2	0.852	1
						RGPAPTLAQAAGSCR	2	0.9465	2
Q5993-1	Q96BW5-2	PTER_HUMAN	PTER	Isoform 2 of Phosphotriesterase-related protein	0.9903	9.27	2	2	2
Q5993-2	Q96BW5	PTER_HUMAN	PTER	Phosphotriesterase-related protein	0.9903	8.02	2	2	2
						CGIIGEGCSWPLTESER	2	0.8447	1
						LLVEEGCEDR	2	0.9373	1
Q5994-1	Q96DG6	CMBL_HUMAN	CMBL	Carboxymethylenebutenolidase homolog	1.0000	13.47	3	1	8
						AVIVIQDIFGWLPNTR	3	0.9996	4
						AVIVIQDIFGWLPNTR	3	0.9994	2
						EVQVEHIK	2	0.9938	1
						LEYGLGR	2	0.9965	1
Q5995-1	Q96HJ9-2	CG055_HUMAN	C7orf55	Isoform 2 of UPF0562 protein C7orf55	1.0000	3.71	2	2	3
Q5995-2	Q9Y383-2	LC7L2_HUMAN	LUC7L2	Isoform 2 of Putative RNA-binding protein Luc7-like 2	1.0000	4.35	2	2	3
Q5995-3	Q9Y383-3	LC7L2_HUMAN	LUC7L2	Isoform 3 of Putative RNA-binding protein Luc7-like 2	1.0000	4.37	2	2	3
Q5995-4	Q9Y383	LC7L2_HUMAN	LUC7L2	Putative RNA-binding protein Luc7-like 2	1.0000	4.34	2	2	3
						VHDLALR	2	0.99	1
						VHLENEIGK	2	0.9956	2
Q5996-1	Q96HR3-2	MED30_HUMAN	MED30	Isoform 2 of Mediator of RNA polymerase II transcription subunit 30	0.9597	6.29	1	1	2
Q5996-2	Q96HR3	MED30_HUMAN	MED30	Mediator of RNA polymerase II transcription subunit 30	0.9597	5.06	1	1	2
						TMEIFOLLR	2	0.9597	2
Q5997-1	Q96IY4	CPB2_HUMAN	CPB2	Carboxypeptidase B2	1.0000	7.57	3	3	5
						DTGTGYLLPER	2	0.9835	3
						EFAFAVSK	2	0.8309	1
						NAIWIDCGIHAR	2	0.8319	1
Q5998-1	Q96KP4	CNDP2_HUMAN	CNDP2	Cytosolic non-specific dipeptidase	1.0000	36.42	11	12	19
						EGGSIPVTLTQEATGK	2	0.9995	2
						FCLGEMESGSGDELIFAR	2	0.9997	3
						FCLGEMESGSGDELIFAR	3	0.9698	1
						GSTDQKGPVAGWINALEAYQK	3	0.992	2
						LYDDIDFIEFAK	2	0.9917	1
						MLAALYEVSQLKD	3	0.9906	1
						MMEVAAADVVK	2	0.999	1
						QKLPGSEIRPPNLLGR	3	0.9953	4
						TGQEIPIVNR	2	0.9962	1
						TVCYIYGLDVOPALEGDWSEPTLVER	3	0.9869	1
						TVFGVEPLTR	2	0.9976	1
						YNYIEGTR	2	0.9959	1
Q5999-1	Q96QE3	ATAD5_HUMAN	ATAD5	ATPase family AAA domain-containing protein 5	0.9965	1.46	2	2	2
						KVPPSPKSSGPK	2	0.9004	1
						SEATDGGFTSQIRK	2	0.9649	1
Q51000-1	Q96QK1	VPS35_HUMAN	VPS35	Vacuolar protein sorting-associated protein 35	1.0000	3.89	2	3	4
						AQLAANTLIIGTFER	2	0.9997	2
						LFDFISQQVATVIQSR	2	0.9985	1
						LFDFISQQVATVIQSR	3	0.9331	1
Q51001-1	Q96TA1-2	NIBL1_HUMAN	FAM129B	Isoform 2 of Niban-like protein 1	1.0000	2.86	2	2	3
Q51001-2	Q96TA1	NIBL1_HUMAN	FAM129B	Niban-like protein 1	1.0000	2.82	2	2	3
						FQVSTSVFK	2	0.985	1
						FQELIFEDFAR	2	0.9996	2
Q51002-1	Q99832-3	TCPH_HUMAN	CTT7	Isoform 3 of T-complex protein 1 subunit eta	1.0000	16.03	6	6	9
Q51002-2	Q99832	TCPH_HUMAN	CTT7	T-complex protein 1 subunit eta	1.0000	14.73	6	6	9
						CQVFEETQIGGER	2	0.9996	2
						GGAEQFMEETER	2	0.9606	1
						IALLNVELEK	2	0.9824	1
						INALTAASEAACLVSVDETINKNPR	3	0.9993	3
						LLDVVHPAAK	2	0.8255	1
						YNFFTGCCK	2	0.9076	1
Q51003-1	Q99988	GDF15_HUMAN	GDF15	Growth/differentiation factor 15	1.0000	10.39	2	2	5
						ASLEDGLWADWVLSRP	2	0.9996	3
						TDTGVSLQTYDOLLAK	2	0.9996	2
Q51004-1	Q98R76	COR1B_HUMAN	CORO1B	Coronin-1B	1.0000	16.16	5	5	11
						AGEAGKLEEVMOQLR	3	0.9974	2
						KCEPIVMTVPR	2	0.9732	2
						KSOLFDDLYPDTAGPEALAEAEVWSGR	3	0.9988	3
						VGIIAHHPTAR	3	0.9992	2
						VTWDSITFCVAVNPK	2	0.9996	2
Q51005-1	Q98RK3-4	MXRAB_HUMAN	MXRAB	Isoform 4 of Matrix-remodeling-associated protein 8	1.0000	6.74	2	2	5
						HVEEAQQVVHWDR	3	0.9996	2
						VAVGADAFER	2	0.9986	3
Q51006-1	Q98RK3-2	MXRAB_HUMAN	MXRAB	Isoform 2 of Matrix-remodeling-associated protein 8	1.0000	28.89	13	17	30
Q51006-2	Q98RK3-3	MXRAB_HUMAN	MXRAB	Isoform 3 of Matrix-remodeling-associated protein 8	1.0000	30.02	13	17	30
Q51006-3	Q98RK3	MXRAB_HUMAN	MXRAB	Matrix-remodeling-associated protein 8	1.0000	29.41	13	17	30
						AYGPIFLR	2	0.9996	2
						DRVAVGADAFER	2	0.9602	2
						HVEEAQQVVHWDR	2	0.9997	3
						HVEEAQQVVHWDR	3	0.9996	2
						HVEEAQQVVHWDRQPPGVPHDR	3	0.832	1
						LEVTDGPPATPAYWDGEKVLAVAR	3	0.9895	1
						LLDLYASGERR	2	0.9443	1
						LLDLYSAGEQR	2	0.9997	4
						RLDLYSAGEQR	2	0.9978	2
						RVFHLTVAEHPAEPPPR	3	0.9638	1
						RVFHLTVAEHPAEPPPR	4	0.8589	1
						SSVVSSEAVSWAGAR	2	0.8566	1
						VAVGADAFER	2	0.9986	3
						VFHLTVAEHPAEPPPR	2	0.9992	1
						VFHLTVAEHPAEPPPR	3	0.9992	3
						VFHLTVAEHPAEPPPR	4	0.8844	1
						VLHWDLR	2	0.9938	1
Q51007-1	Q98RL6-2	SRSF8_HUMAN	SRSF8	Isoform 2 of Serine/arginine-rich splicing factor 8	0.9991	2.91	1	1	1
Q51007-2	Q98RL6	SRSF8_HUMAN	SRSF8	Serine/arginine-rich splicing factor 8	0.9991	2.84	1	1	1
						VGDDVYIPR	2	0.9789	1
Q51008-1	Q98T78-2	CSN4_HUMAN	COPS4	Isoform 2 of COP9 signalosome complex subunit 4	1.0000	9.09	2	3	4
						CQQLAAYGILEK	2	0.857	1
						LYNNITFEELGALLEIPAAK	2	0.9994	1
						LYNNITFEELGALLEIPAAK	3	0.999	2
Q51009-1	Q98T70	AN32E_HUMAN	ANP32E	Acidic leucine-rich nuclear phosphoprotein 32 family member 3	1.0000	13.06	2	2	3
Q51009-2	Q98T70-3	AN32E_HUMAN	ANP32E	Isoform 3 of Acidic leucine-rich nuclear phosphoprotein 32 family member 3	1.0000	15.91	2	2	3
						KLEIFSDNIISGGLVLAEK	3	0.9965	2
						SLDLNFCEITNLEDYR	2	0.9963	1

Q51010-1	Q9BUF5	TB86_HUMAN	TUBB6	Tubulin beta-6 chain	1.0000	18.83	6	6	12
						EIVHIQAGCCNQIGTK	3	0.8277	1
						FWEVISDEHGIDPAGGYGDSALQLER	3	0.999	4
						GHYTEGAELVDVLDVVR	3	0.9989	3
						GHYTEGAELVDVLDVVRK	3	0.9891	1
						INVYNESSSQK	2	0.9995	2
Q51011-1	Q9BUT1	BDH2_HUMAN	BDH2	3-hydroxybutyrate dehydrogenase type 2	1.0000	13.47	2	2	5
						SVAADFIQGGIR	2	0.9994	2
						VIILTAAAGQGQAAALAFAR	3	0.9996	3
Q51012-1	Q9BVA1	TB82B_HUMAN	TUBB2B	Tubulin beta-2B chain	1.0000	18.65	4	4	9
						ALTVPELTQQMFDSK	2	0.9952	3
						ESESCDCLQGFQLTSLGGGTSGMGTLISK	3	0.9946	1
						FWEVISDEHGIDPTGSHYHGDSDLQLER	3	0.9981	3
						YLTVAIFR	2	0.9989	2
Q51013-1	Q9H223	EHD4_HUMAN	EHD4	EH domain-containing protein 4	1.0000	10.54	5	5	10
						AGGADAVQTVTGGLR	2	0.9996	3
						EYQISAGDFFPEVK	2	0.9997	2
						FGNAFLNR	2	0.996	1
						LPEYIQLQR	2	0.9873	1
						YLLEQDFPGMR	2	0.9995	3
Q51014-1	Q9H3G5	CPVL_HUMAN	CPVL	Probable serine carboxypeptidase CPVL	1.0000	15.55	6	7	16
						CTEPEDQLYYK	2	0.9991	4
						DLYSALIQFFQIFPEYK	2	0.9997	3
						DLYSALIQFFQIFPEYK	3	0.9996	3
						FLSLPEVR	2	0.9886	2
						GGGHILPYDQPLR	3	0.9969	1
						NNDFYVTGESYAGK	2	0.9997	2
						SSEVAGYIR	2	0.9991	1
Q51015-1	Q9H4A4	AMPB_HUMAN	RNPEP	Aminopeptidase B	1.0000	12.31	7	7	9
						AEFGPPGPGAGSR	2	0.9907	1
						AFELAHHL	3	0.8938	1
						CLEFEGAAELR	2	0.8422	1
						GLSGTAVDLR	2	0.9983	2
						ISTILFGAAYTCLEATGR	3	0.9104	1
						LFGPPYVWGR	2	0.9301	1
						LQVLLTYR	2	0.9681	2
Q51016-1	Q9H4G0	E41L1_HUMAN	EPB41L1	Band 4.1-like protein 1	1.0000	6.7	3	3	5
Q51016-2	Q9H4G0-2	E41L1_HUMAN	EPB41L1	Isoform 2 of Band 4.1-like protein 1	1.0000	7.57	3	3	5
Q51016-3	Q9H4G0-4	E41L1_HUMAN	EPB41L1	Isoform 4 of Band 4.1-like protein 1	1.0000	8.42	3	3	5
						DVLSTYGATAETLSTTTHTVK	3	0.9683	2
						HIITGDEDVDQDALAIK	2	0.9979	1
						VTLLDASEYCEVEK	2	0.9995	2
Q51017-1	Q9H8L6	MMRN2_HUMAN	MMRN2	Multimerin-2	0.9631	1.37	1	1	3
						VWFELTQSSITKR	2	0.9631	3
Q51018-1	Q9HAT2-2	SIAE_HUMAN	SIAE	Isoform 2 of Sialate O-acetyltransferase	0.9999	5.94	2	2	2
Q51018-2	Q9HAT2	SIAE_HUMAN	SIAE	Sialate O-acetyltransferase	0.9999	5.54	2	2	2
						FFPFGVLQSLSDLSK	2	0.9945	1
						WHQTADFGVYPNPK	3	0.9886	1
Q51019-1	Q9H840	RISC_HUMAN	SCPEP1	Retinoid-inducible serine carboxypeptidase	1.0000	3.76	2	2	2
						EATELWKG	2	0.9457	1
						NLAFYWILK	2	0.9867	1
Q51020-1	Q9HD89	RETN_HUMAN	RETN	Resistin	1.0000	24.07	3	3	7
						AISSIGLEQSVTSR	2	0.9997	2
						IQEAVGSLFR	2	0.9996	3
						SSIGLEQSVTSR	2	0.9431	2
Q51021-1	Q9NQ78	KI13B_HUMAN	KIF13B	Kinesin-like protein KIF13B	0.9999	1.2	2	2	4
						SVLAVENTLLDR	2	0.9992	2
						YAGQDIVFK	2	0.9223	2
Q51022-1	Q9NRX4	PHP14_HUMAN	PHPT1	14 kDa phosphohistidine phosphatase	1.0000	43.2	3	3	6
						AKYPDYEVTWANDGY	2	0.9983	2
						IHYGYSMAGPAQHAISTEK	3	0.9996	3
						WAEYHADIYKVSQDMQK	3	0.9827	1
Q51023-1	Q9NSB2	KRT84_HUMAN	KRT84	Keratin, type II cuticular Hb4	1.0000	1.33	1	1	1
						AQYEEVAR	2	0.982	1
Q51024-1	Q9NZ45	CISD1_HUMAN	CISD1	CDGSH iron-sulfur domain-containing protein 1	0.9491	13.89	1	1	1
						HNEETGDNVGPLIK	2	0.9491	1
Q51025-1	Q9NZ66	Q9NZ66_HUMAN	EIF4A2	Eukaryotic initiation factor 4A-II	1.0000	3.21	1	1	3
						VLTITDILAR	2	0.9995	3
Q51026-1	Q9NZW4	DSPP_HUMAN	DSPP	Dentin sialophosphoprotein	0.9525	1.92	1	1	1
						SDSSSSSSSSDSTSSNDSQSK	2	0.8143	1
Q51027-1	Q9P258	RCC2_HUMAN	RCC2	Protein RCC2	1.0000	6.32	4	4	6
						AQRIEYDCELVR	3	0.9224	1
						AVQDLGWR	2	0.9971	1
						IYDCELVR	2	0.9978	2
						VFSWGGGYYGR	2	0.9962	2
Q51028-1	Q9P260-2	K1468_HUMAN	KIAA1468	Isoform 2 of Lish domain and HEAT repeat-containing protein KIAA1468	1.0000	2.48	2	2	4
Q51028-2	Q9P260	K1468_HUMAN	KIAA1468	Lish domain and HEAT repeat-containing protein KIAA1468	1.0000	2.55	2	2	4
						DQYLLTALEHTELLESGR	3	0.9727	2
						LSIDAIAAQLLR	2	0.9992	2
Q51029-1	Q9UBF2	COPG2_HUMAN	COPG2	Coatomer subunit gamma-2	0.9999	1.38	1	1	2
						SIATLAITLLK	2	0.9967	2
Q51030-1	Q9UBQ7	GRHPR_HUMAN	GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	1.0000	8.23	2	2	3
Q51030-2	U3KQ56	U3KQ56_HUMAN	GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	1.0000	7.54	2	2	3
						GDVVNQDDLYQALASGK	2	0.9994	2
						ILDAAGANLK	2	0.9845	1
Q51031-1	Q9UBR2	CATZ_HUMAN	CTS2	Cathepsin Z	1.0000	15.84	4	4	7
						NSWGEPPWGER	2	0.9962	1
						NVDGVNYASITR	2	0.9993	2
						VDGYSLSGR	2	0.9993	1
						YNLAIEHCTFGDPV	2	0.9995	3
Q51032-1	Q9UDV7	ZN282_HUMAN	ZN282	Zinc finger protein 282	0.9909	7	1	1	1
						GSGEAPPGDGRSTGGGGGGGGGGAAGTAGGGCGSCCPGLRR	3	0.9553	1
Q51033-1	Q9UDY2-6	ZO2_HUMAN	TJP2	Isoform 6 of Tight junction protein ZO-2	1.0000	9.85	8	9	16
Q51033-2	Q9UDY2-7	ZO2_HUMAN	TJP2	Isoform 7 of Tight junction protein ZO-2	1.0000	9.34	8	9	16
Q51033-3	Q9UDY2-2	ZO2_HUMAN	TJP2	Isoform A2 of Tight junction protein ZO-2	1.0000	10.93	8	9	16
Q51033-4	Q9UDY2-5	ZO2_HUMAN	TJP2	Isoform A3 of Tight junction protein ZO-2	1.0000	11.48	8	9	16
Q51033-5	Q9UDY2-3	ZO2_HUMAN	TJP2	Isoform C1 of Tight junction protein ZO-2	1.0000	9.77	8	9	16
Q51033-6	Q9UDY2-4	ZO2_HUMAN	TJP2	Isoform C2 of Tight junction protein ZO-2	1.0000	11.18	8	9	16
Q51033-7	Q9UDY2	ZO2_HUMAN	TJP2	Tight junction protein ZO-2	1.0000	9.58	8	9	16
						EDAVLYLLEIPK	2	0.9996	2
						GDFFIR	2	0.9584	1
						GLVREDAVLYLLEIPKGMVTLAQSR	3	0.9388	1
						GLVREDAVLYLLEIPKGMVTLAQSR	4	0.9885	3
						LAGGNDYGFVAGIQEGTSAEQGLQEGDQILK	3	0.9987	3
						LANELPDWFGITAK	2	0.9895	1
						LQNIWAVR	2	0.9964	2
						SHFECEKETPOSIAFTR	3	0.9958	2
						VVDITLYGDK	2	0.9764	1
Q51034-1	Q9UEW8	STK39_HUMAN	STK39	STE20/SPS1-related proline-alanine-rich protein kinase	1.0000	9.17	3	3	7
						DAYLEQEVIGSGATVAQOALCKPR	3	0.9994	4
						LASGCDGSEIPDEVK	2	0.9986	2
						LIGFAQLSVS	2	0.9849	1
Q51035-1	Q9UGIO	ZRAN1_HUMAN	ZRAN1	Ubiquitin thioesterase ZRAN1	0.9741	1.41	1	1	1
						GSCSGNSQR	2	0.9549	1
Q51036-1	Q9UGM5	FETUB_HUMAN	FETUB	Fetuin-B	0.9641	2.88	1	1	1
						IFFESVYGQCK	2	0.9641	1
Q51037-1	Q9UGT4	SUSD2_HUMAN	SUSD2	Sushi domain-containing protein 2	0.9797	4.74	2	2	3
						CGALDGPSCSHPTCSGLGTCCLDLR	3	0.9509	2
						GETVLLAALTDLR	2	0.9797	1
Q51038-1	Q9UHB9-2	SRP68_HUMAN	SRP68	Isoform 2 of Signal recognition particle subunit SRP68	1.0000	2.18	1	1	2
Q51038-2	Q9UHB9-3	SRP68_HUMAN	SRP68	Isoform 3 of Signal recognition particle subunit SRP68	1.0000	4.51	1	1	2
						FETFCLDPLSLVTK	2	0.9983	2

Q51039-1	Q9UHB9-4	SRP68_HUMAN	SRP68	Isoform 4 of Signal recognition particle subunit SRP68	1.0000	10.19	3	3	4
Q51039-2	Q9UHB9	SRP68_HUMAN	SRP68	Signal recognition particle subunit SRP68	1.0000	9.57	3	3	4
						FETFCLDPSLVTK	2	0.9983	2
						KQVPGGGGGGGGGGGGGGGGGGGR	2	0.8463	1
						SGGTGLLAEKLEALITQTR	3	0.9664	1
Q51040-1	Q9UHD8-2	SEPT9_HUMAN	SEPT9	Isoform 2 of Septin-9	0.9994	3.87	1	1	2
Q51040-2	Q9UHD8-5	SEPT9_HUMAN	SEPT9	Isoform 5 of Septin-9	0.9994	3.8	1	1	2
Q51040-3	Q9UHD8-7	SEPT9_HUMAN	SEPT9	Isoform 7 of Septin-9	0.9994	3.88	1	1	2
Q51040-4	Q9UHD8	SEPT9_HUMAN	SEPT9	Septin-9	0.9994	3.75	1	1	2
						TELSIDISSKQVENAGAIGPSR	2	0.9241	2
Q51041-1	Q9UIB8-2	SLAF5_HUMAN	CD84	Isoform 2 of SLAM family member 5	1.0000	11.21	2	2	4
Q51041-2	Q9UIB8-3	SLAF5_HUMAN	CD84	Isoform 3 of SLAM family member 5	1.0000	11.59	2	2	4
Q51041-3	Q9UIB8-4	SLAF5_HUMAN	CD84	Isoform 4 of SLAM family member 5	1.0000	13.57	2	2	4
Q51041-4	Q9UIB8-5	SLAF5_HUMAN	CD84	Isoform 5 of SLAM family member 5	1.0000	13.97	2	2	4
Q51041-5	Q9UIB8-6	SLAF5_HUMAN	CD84	Isoform 6 of SLAM family member 5	1.0000	15.77	2	2	4
Q51041-6	Q9UIB8	SLAF5_HUMAN	CD84	SLAM family member 5	1.0000	11.01	2	2	4
						IHALGPNYNLVISDLR	3	0.9991	2
						TSVAVYTPGDSETAIPVVTVTHR	3	0.9941	2
Q51042-1	Q9UIJ70-2	NAGK_HUMAN	NAGK	Isoform 2 of N-acetyl-D-glucosamine kinase	1.0000	11.03	2	2	3
						DANGGTSSDGSSSMAAYGGVEGGGTR	3	0.9273	1
						SLGLSLSGGQDQDAGR	2	0.9996	2
Q51043-1	Q9UIJ72	ANX10_HUMAN	ANX10	Annexin A10	1.0000	7.72	2	2	5
						GVGTDCNLEILASR	2	0.9991	3
						SEIDLLTIR	2	0.9965	2
Q51044-1	Q9UKU9	ANGL2_HUMAN	ANGPTL2	Angiotensin-related protein 2	1.0000	23.12	9	11	16
						DCLQALEDGHDTSSILVKPENTNR	3	0.9712	1
						HDPGGWTVIQR	2	0.9781	1
						KVFAEYASFR	2	0.9975	1
						KVFAEYASFR	3	0.9943	2
						LDGSVNFR	2	0.9986	2
						LLVTMEDWSGR	2	0.9996	2
						LMQYVWCQR	2	0.9957	1
						QSGFNIDGGEYWLLENYWLITNQGNKY	3	0.9522	1
						RLDGSVNFR	2	0.9979	2
						RLDGSVNFR	3	0.9979	2
						YQDGVYWAER	2	0.9353	1
Q51045-1	Q9UL46	PSME2_HUMAN	PSME2	Proteasome activator complex subunit 2	0.9999	12.97	2	2	3
						AFYAELYHIISNLEK	3	0.9687	1
						ALVHERDEAAYGELR	3	0.8949	2
Q51046-1	Q9UN67	PCDBA_HUMAN	PCDH810	Protocadherin beta-10	0.9472	1.63	1	1	1
Q51046-2	Q9Y5E6	PCDB3_HUMAN	PCDH83	Protocadherin beta-3	0.9472	1.63	1	1	1
Q51046-3	Q9Y5E5	PCDB4_HUMAN	PCDH84	Protocadherin beta-4	0.9472	1.64	1	1	1
Q51046-4	Q9Y5E4	PCDB5_HUMAN	PCDH85	Protocadherin beta-5	0.9472	1.64	1	1	1
Q51046-5	Q9Y5E2	PCDB7_HUMAN	PCDH87	Protocadherin beta-7	0.9472	1.64	1	1	1
Q51046-6	Q9UN66	PCDB8_HUMAN	PCDH88	Protocadherin beta-8	0.9472	1.62	1	1	1
						SLDYALQAFEFR	2	0.9472	1
Q51047-1	Q9UN70-2	PCDGC_HUMAN	PCDHGC3	Isoform 2 of Protocadherin gamma-C3	1.0000	4.52	3	3	3
Q51047-2	Q9UN70	PCDGC_HUMAN	PCDHGC3	Protocadherin gamma-C3	1.0000	4.18	3	3	3
						GFAVGNVAVNLGLDLGSLSR	2	0.9956	1
						VLEDAPSSTR	2	0.9675	1
						YAEVLVR	2	0.9956	1
Q51048-1	Q9UNN8	EPCR_HUMAN	PROCR	Endothelial protein C receptor	0.9988	5.46	1	1	1
						EFLEDTCVQYVQK	2	0.9651	1
Q51049-1	Q9Y287	ITM2B_HUMAN	ITM2B	Integral membrane protein 2B	0.9735	3.76	1	1	1
						NLLELLINIK	2	0.9735	1
Q51050-1	Q9Y252-2	CRYL1_HUMAN	CRYL1	Isoform 2 of Lambda-crystallin homolog	1.0000	15.44	4	4	7
Q51050-2	Q9Y252	CRYL1_HUMAN	CRYL1	Lambda-crystallin homolog	1.0000	14.42	4	4	7
						NHLOTQGPPEFSR	3	0.9913	2
						IFAQDSIIDDR	2	0.9994	2
						LFAGLVHVK	2	0.9992	1
						LQYAISEAWR	2	0.9997	2
Q51051-1	Q9Y277	YBOX2_HUMAN	YBX2	Y-box-binding protein 2	0.9957	18.13	2	2	2
						AGATAVPAATVPATAAGVVAVVPVPAPEPQKGGAGGGGAASGPAAGTPSAPGSR	5	0.8305	1
						MSEVEAAAGATAVPAATVPATAAGVVAVVPVPAPEPQKGGAGGGGAASGPAAGTPSAPGSRTP	5	0.9745	1
Q51052-1	Q9Y2X9-2	ZN281_HUMAN	ZN281	Isoform 2 of Zinc finger protein 281	0.9857	4.54	2	2	2
Q51052-2	Q9Y2X9	ZN281_HUMAN	ZN281	Zinc finger protein 281	0.9857	4.36	2	2	2
						MKIGSGFLSGGGGTGSGGGSGGGGGGGGGGGSSGR	3	0.9219	1
						MKIGSGFLSGGGGTGSGGGSGGGGGGGGGGGSSGR	3	0.8173	1
Q51053-1	Q9Y2Y8	PRG3_HUMAN	PRG3	Proteoglycan 3	1.0000	35.56	5	6	11
						CYGGNLSYSHDFNFNFR	2	0.9996	3
						CYGGNLSYSHDFNFNFR	3	0.9987	1
						FCWTDGSHWNFAWSPGQNGGQSCVALCTK	3	0.8941	1
						IQCCSTVNQAQVWIGGNLR	3	0.9978	3
						TFAEAQNVCSR	2	0.9996	2
						TSTVNOAQVWIGGNLR	2	0.9404	1
Q51054-1	Q9Y5H0-2	PCDG3_HUMAN	PCDHGA3	Isoform 2 of Protocadherin gamma-A3	0.9312	1.21	1	1	1
Q51054-2	Q9Y5H0	PCDG3_HUMAN	PCDHGA3	Protocadherin gamma-A3	0.9312	1.07	1	1	1
						LEKSIDQYR	2	0.8911	1
Q51055-1	Q9Y678	COPG1_HUMAN	COPG1	Coatamer subunit gamma-1	1.0000	3.43	2	2	3
						SIATLAITLLK	2	0.9967	2
						SSPEPVALTETEVYIR	2	0.9986	1
Q51056-1	R4GMN6	R4GMN6_HUMAN	C1R	Complement C1r subcomponent (Fragment)	1.0000	10.32	2	2	5
						LPVANPOACENWLR	2	0.9983	3
						WVATGIVSWGIGCSR	2	0.9985	2
Q51057-1	R4GN69	R4GN69_HUMAN	HSPH1	Heat shock protein 105 kDa	1.0000	12.17	1	1	3
						AGGIETIANEFSR	2	0.9994	3
Q51058-1	R4GN98	R4GN98_HUMAN	S100A6	Protein S100-A6 (Fragment)	0.9991	9.41	1	1	2
						LQDAEIR	2	0.9901	2
Q51059-1	V9GYE3	V9GYE3_HUMAN	APOA2	Apolipoprotein A-II	1.0000	84.62	4	5	11
						AGTELVNLSYFVLTGPATQ	3	0.9994	3
						SKEQLTPLIK	2	0.9958	1
						SKEQLTPLIK	2	0.9656	1
						VKSPQLQAEAK	2	0.9994	4
						VKSPQLQAEAK	3	0.9979	2
Q51060-1	V9GYZ6	V9GYZ6_HUMAN	EPRS	Bifunctional glutamate/proline-tRNA ligase (Fragment)	1.0000	2.79	2	2	5
						GFICDQPEYPSYPSCK	2	0.9996	3
						KGDHQLQR	2	0.9975	2
Q51061-1	X6R2L4	X6R2L4_HUMAN	RUVBL2	RuvB-like 2	1.0000	5.02	1	1	2
						TTMETIYDLGTK	2	0.9976	2
Q51062-1	X6RLJ0	X6RLJ0_HUMAN	C1QA	Complement C1q subcomponent subunit A (Fragment)	0.9997	4.55	1	1	1
						SLGFCDTTNK	2	0.997	1

----- Summary -----	
Total Peptides:	5,957
Total Proteins:	2,468
Total Groups (Q#):	1,062
Total Groups (W#):	1,071
Total Genes:	893
Total Proteins in the Database:	177,988
Total Genes in the Database:	25,200
Protein Quantification Rate (%):	1.387
Gene Quantification Rate (%):	3.544